



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 160284

TO: Patricia Duffy
Location: REM-3B05/3C18
Art Unit: 1645
Thursday, July 28, 2005

Case Serial Number: 09/900766

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

Examiner Duffy,

Please review the attached search results.

If you have any questions or if you would like to refine the search query, please feel free to contact me at any time.

Thank you for using STIC search services!

Paul Schulwitz
Technical Information Specialist
REM-1A65
571-272-2527



This Page Blank (uspto)

160284

From: Duffy, Patricia
Sent: Friday, July 22, 2005 6:51 PM
To: STIC-Biotech/ChemLib
Subject: sequence search 09/900,766

Importance: High

In RE: 09/900,766

Please search SEQ ID NO:7 in commercial and interference databases.
Please print out top 100 hits in each category.

Thanks mucho.

Patricia A. Duffy, Ph.D.
Art Unit 1645
Remsen 3B05; Mailbox 3C18
571-272-0855

STAFF USE ONLY

Searcher: _____
 Searcher Phone: 2-_____
 Date Searcher Picked up: _____
 Date Completed: 7/18
 Searcher Prep/Rev. Time: _____
 Online Time: _____

Type of Search

NA#: _____ AA#: _____
Interference: _____ SPDI: _____
S/L: _____ Oligomer: _____
Encode/Transl: _____
Structure#: _____ Text: _____
Inventor: _____ Litigation: _____

Vendors and cost where applicable
STN: _____
DIALOG: _____
QUESTEL/ORBIT: _____
LEXIS/NEXIS: _____
SEQUENCE SYSTEM: _____
WWW/Internet: _____
Other(Specify): _____

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 11:08:35 ; Search time 159 Seconds
(without alignments)
570.033 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKDLRKSELR.....RDNTKINSENLHLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1741741 seqs, 388992284 residues

Total number of hits satisfying chosen parameters: 1741741

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep.*
- 12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 13: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	10	US-09-900-766-7
2	1238	100.0	233	14	US-10-283-838-8
3	1238	100.0	257	15	US-10-267-682-112
4	1238	100.0	257	15	US-10-267-748-112
5	1238	100.0	257	16	US-10-428-817A-188
6	1210	97.7	233	10	US-09-900-766-3
7	1188	96.0	248	9	US-09-870-759-16
8	1188	96.0	248	10	US-09-751-708A-16
9	1188	96.0	248	16	US-10-428-817A-12
10	1188	96.0	248	17	US-10-937-758A-16
11	1107	89.4	233	10	US-09-900-766-2
					Sequence 7, Appli
					Sequence 8, Appli
					Sequence 112, App
					Sequence 112, App
					Sequence 188, App
					Sequence 3, Appli
					Sequence 16, Appl
					Sequence 16, Appl
					Sequence 12, Appl
					Sequence 16, Appl
					Sequence 2, Appli

1107	89.4	672	10	US-09-900-766-1	Sequence 1, Appli
1023	82.6	233	10	US-09-900-766-4	Sequence 4, Appli
1023	82.6	233	14	US-10-283-838-7	Sequence 7, Appli
1023	82.6	257	15	US-10-267-682-113	Sequence 113, App
1023	82.6	257	15	US-10-267-748-113	Sequence 113, App
1019	82.3	233	15	US-10-354-948-4	Sequence 4, Appli
1013	81.8	257	9	US-09-870-759-8	Sequence 8, Appli
1013	81.8	257	10	US-09-751-708A-8	Sequence 8, Appli
1013	81.8	257	16	US-10-428-817A-4	Sequence 4, Appli
1013	81.8	257	17	US-10-937-758A-8	Sequence 8, Appli
1000	80.8	257	14	US-10-002-784A-2	Sequence 2, Appli
1000	80.8	257	17	US-10-767-687-2	Sequence 2, Appli
996	80.5	233	14	US-10-002-784A-4	Sequence 4, Appli
991	80.0	233	17	US-10-767-687-4	Sequence 4, Appli
983	79.4	257	8	US-08-882-431-2	Sequence 8, Appli
978	79.0	233	8	US-08-882-431-4	Sequence 2, Appli
921	74.4	227	18	US-10-997-690-11	Sequence 11, Appl
830	67.0	268	16	US-10-428-817A-175	Sequence 175, App
663	53.6	258	9	US-09-870-759-14	Sequence 14, Appl
663	53.6	258	10	US-09-751-708A-14	Sequence 14, Appl
663	53.6	258	16	US-10-428-817A-10	Sequence 10, Appl
663	53.6	258	16	US-10-428-817A-174	Sequence 174, App
663	53.6	258	16	US-10-428-817A-177	Sequence 177, App
663	53.6	258	17	US-10-937-758A-14	Sequence 14, Appl
523	42.2	203	10	US-09-900-766-5	Sequence 5, Appli
457	36.9	82	14	US-10-002-784A-34	Sequence 34, Appl
399	32.2	82	17	US-10-767-687-19	Sequence 19, Appl
399	32.2	82	17	US-10-767-687-17	Sequence 17, Appl
366	29.6	217	10	US-09-900-766-6	Sequence 6, Appli
366	29.6	217	16	US-10-428-817A-173	Sequence 173, App
343.5	27.7	259	16	US-10-474-792-416	Sequence 416, App
339.5	27.4	242	16	US-10-428-817A-174	Sequence 174, App
337	27.2	240	16	US-10-428-817A-177	Sequence 177, App
320	25.8	239	16	US-10-428-817A-178	Sequence 178, App
319.5	25.8	242	16	US-10-428-817A-172	Sequence 172, App
310	25.0	242	16	US-10-428-817A-176	Sequence 176, App
300.5	24.3	266	9	US-09-870-759-10	Sequence 10, Appl
300.5	24.3	266	10	US-09-751-708A-10	Sequence 10, Appl
300.5	24.3	266	16	US-10-428-817A-6	Sequence 6, Appli
300.5	24.3	266	17	US-10-937-758A-10	Sequence 10, Appl
300	24.2	255	15	US-10-354-948-2	Sequence 2, Appli
299.5	24.2	238	16	US-10-428-817A-183	Sequence 183, App
299.5	24.2	239	9	US-09-150-947B-12	Sequence 12, Appl
299.5	24.2	239	14	US-10-172-425B-12	Sequence 12, Appl
299.5	23.9	251	16	US-10-428-817A-163	Sequence 163, App
294.5	23.8	251	8	US-08-973-391A-13	Sequence 13, Appl
294.5	23.8	251	9	US-09-308-830-13	Sequence 13, Appl
293.5	23.7	240	17	US-10-923-324-4	Sequence 4, Appli
293.5	23.7	266	14	US-10-002-784A-6	Sequence 6, Appli
293.5	23.7	266	17	US-10-767-687-6	Sequence 6, Appli
292.5	23.6	266	14	US-10-151-336-8	Sequence 8, Appli
289.5	23.4	251	8	US-08-882-431-16	Sequence 16, Appl
289.5	23.4	251	14	US-10-002-784A-16	Sequence 16, Appl
289.5	23.4	251	17	US-10-767-687-16	Sequence 16, Appl
288.5	23.3	239	14	US-10-002-784A-10	Sequence 10, Appl
288.5	23.3	239	17	US-10-767-687-10	Sequence 10, Appl
288.5	23.3	240	17	US-10-923-324-3	Sequence 3, Appli
287.5	23.2	239	8	US-08-882-431-10	Sequence 10, Appl
287.5	23.2	240	17	US-10-923-324-6	Sequence 6, Appli
287.5	23.1	240	17	US-10-923-324-5	Sequence 5, Appli
285.5	22.9	266	16	US-10-428-817A-186	Sequence 186, App
285.5	22.9	240	17	US-10-923-324-2	Sequence 2, Appli
285.5	22.8	266	14	US-10-002-784A-8	Sequence 8, Appli
285.5	22.8	266	17	US-10-767-687-8	Sequence 8, Appli
285.5	22.7	239	16	US-10-428-817A-185	Sequence 185, App
280	22.6	265	8	US-08-882-431-6	Sequence 6, Appli
276.5	22.3	240	17	US-10-923-324-7	Sequence 7, Appli
276.5	22.3	240	17	US-10-923-324-8	Sequence 8, Appli
276.5	22.3	265	8	US-08-882-431-8	Sequence 8, Appli
276.5	22.3	260	16	US-10-428-817A-171	Sequence 171, App
266.5	21.5	266	9	US-09-870-759-12	Sequence 12, Appl
266.5	21.5	266	10	US-09-751-708A-12	Sequence 12, Appl

85	266.5	21.5	266	16	US-10-428-817A-8	Sequence 8, Appli	158	96	7.8	227	15	US-10-282-122A-70243	Sequence 70243, A
86	266.5	21.5	266	17	US-10-937-758A-12	Sequence 12, Appl	159	95.5	7.7	616	15	US-10-431-273-59	Sequence 59, Appl
87	265.5	21.4	240	17	US-10-923-324-1	Sequence 1, Appl	160	94.5	7.6	402	18	US-10-724-972A-6144	Sequence 6144, Ap
88	258.5	20.9	266	8	US-08-882-431-14	Sequence 14, Appl	161	94	7.6	226	15	US-10-282-122A-43957	Sequence 43957, A
89	258.5	20.9	266	14	US-10-002-784A-14	Sequence 14, Appl	162	94	7.6	622	15	US-10-425-114-39433	Sequence 39433, A
90	258.5	20.9	266	17	US-10-767-687-14	Sequence 14, Appl	163	94	7.6	622	15	US-10-425-114-60523	Sequence 60523, A
91	256.5	20.7	220	14	US-10-002-784A-26	Sequence 26, Appl	164	93.5	7.6	631	14	US-10-043-344-111	Sequence 11, Appl
92	256.5	20.7	468	14	US-10-002-784A-27	Sequence 27, Appl	165	93	7.5	16	14	US-10-283-838-20	Sequence 20, Appl
93	256	20.7	210	16	US-10-428-817A-170	Sequence 170, App	166	93	7.5	306	15	US-10-425-114-54166	Sequence 54166, A
94	256	20.7	233	16	US-10-937-690-2	Sequence 2, Appli	167	93	7.5	335	16	US-10-425-115-257338	Sequence 257338, A
95	245	19.8	250	9	US-09-870-759-20	Sequence 20, Appl	168	93	7.5	616	15	US-10-431-273-60	Sequence 60, Appl
96	245	19.8	250	10	US-09-751-708A-20	Sequence 20, Appl	169	93	7.5	616	16	US-10-425-115-257343	Sequence 257343, A
97	245	19.8	250	16	US-10-428-817A-16	Sequence 16, Appl	170	93	7.5	618	16	US-10-425-115-257337	Sequence 257337, A
98	245	19.8	250	17	US-10-937-758A-20	Sequence 20, Appl	171	93	7.5	619	16	US-10-425-115-257344	Sequence 257344, A
99	239	19.3	209	16	US-10-428-817A-169	Sequence 169, App	172	93	7.5	643	15	US-10-425-114-38468	Sequence 38468, A
100	220.5	17.8	240	16	US-10-428-817A-184	Sequence 184, App	173	93	7.5	653	15	US-10-425-114-62449	Sequence 62449, A
101	217	17.5	234	16	US-10-474-792-562	Sequence 562, App	174	93	7.5	847	15	US-10-282-122A-59134	Sequence 59134, A
102	217	17.5	234	16	US-10-937-690-4	Sequence 4, Appli	175	92.5	7.5	227	16	US-10-428-817A-193	Sequence 193, App
103	216	17.4	210	16	US-10-428-817A-166	Sequence 166, App	176	90	7.3	463	14	US-10-097-111-288	Sequence 288, App
104	215	17.4	82	14	US-10-002-784A-33	Sequence 33, Appl	177	90	7.3	5005	15	US-10-282-122A-76871	Sequence 76871, A
105	215	17.4	82	17	US-10-767-687-18	Sequence 18, Appl	178	89.5	7.2	612	15	US-10-425-114-63660	Sequence 63660, A
106	197	15.9	204	18	US-10-937-690-22	Sequence 22, Appl	179	89.5	7.2	612	16	US-10-425-115-246981	Sequence 246981, A
107	197	15.9	236	16	US-10-428-817A-167	Sequence 167, App	180	89	7.2	171	15	US-10-282-122A-71154	Sequence 71154, A
108	197	15.9	236	16	US-10-474-792-414	Sequence 414, App	181	89	7.2	179	18	US-10-724-972A-6442	Sequence 6442, Ap
109	197	15.9	236	18	US-10-937-690-6	Sequence 6, Appl	182	89	7.2	516	14	US-10-032-585-7147	Sequence 7147, Ap
110	193	15.6	232	16	US-10-428-817A-168	Sequence 168, App	183	89	7.2	631	14	US-10-043-344-115	Sequence 115, App
111	185	14.9	234	16	US-10-428-817A-165	Sequence 165, App	184	89	7.2	941	15	US-10-369-493-19630	Sequence 19630, A
112	183.5	14.8	235	9	US-09-336-036-2	Sequence 2, Appli	185	89	7.2	1634	15	US-10-435-766-23	Sequence 23, Appl
113	183.5	14.8	235	9	US-09-308-829-2	Sequence 2, Appli	186	89	7.2	1634	17	US-10-734-563-96	Sequence 96, Appl
114	183.5	14.8	235	17	US-10-914-417-2	Sequence 2, Appli	187	89	7.2	1634	18	US-10-853-973A-23	Sequence 23, Appl
115	183.5	14.8	235	17	US-10-914-665-2	Sequence 2, Appli	188	88.5	7.1	308	17	US-10-470-048B-438	Sequence 438, App
116	181.5	14.7	204	18	US-10-937-690-20	Sequence 20, Appl	189	88.5	7.1	313	17	US-10-470-048B-155	Sequence 155, App
117	170	13.7	137	18	US-10-937-690-8	Sequence 8, Appli	190	88	7.1	241	15	US-10-282-122A-70300	Sequence 70300, A
118	159.5	12.9	204	18	US-10-937-690-9	Sequence 9, Appli	191	88	7.1	611	15	US-10-424-599-173518	Sequence 173518, A
119	157	12.7	206	18	US-10-937-690-21	Sequence 21, Appl	192	88	7.1	632	15	US-10-425-114-52842	Sequence 52842, A
120	137.5	11.1	89	14	US-10-002-784A-35	Sequence 35, Appl	193	88	7.1	646	15	US-10-425-114-50103	Sequence 50103, A
121	137.5	11.1	89	14	US-10-767-687-20	Sequence 20, Appl	194	88	7.1	646	15	US-10-425-114-57915	Sequence 57915, A
122	121	9.8	79	17	US-10-002-784A-39	Sequence 39, Appl	195	87.5	7.1	556	15	US-10-282-122A-60731	Sequence 60731, A
123	121	9.8	79	17	US-10-767-687-24	Sequence 24, Appl	196	87.5	7.1	623	15	US-10-425-114-62505	Sequence 62505, A
124	121	9.8	203	18	US-10-937-690-10	Sequence 10, Appl	197	87.5	7.1	1637	16	US-10-437-963-180397	Sequence 180397, A
125	116	9.4	231	16	US-10-428-817A-191	Sequence 191, App	198	87	7.0	286	18	US-10-724-972A-5172	Sequence 5172, Ap
126	114	9.2	231	16	US-10-428-817A-190	Sequence 190, App	199	87	7.0	361	15	US-10-425-114-51445	Sequence 51445, A
127	113	9.1	232	15	US-10-282-122A-70242	Sequence 70242, A	200	87	7.0	384	15	US-10-425-114-51527	Sequence 51527, A
128	112.5	9.1	89	14	US-10-002-784A-37	Sequence 37, Appl	ALIGNMENTS						
129	112.5	9.1	89	14	US-10-002-784A-38	Sequence 38, Appl	RESULT 1						
130	112.5	9.1	89	17	US-10-767-687-22	Sequence 22, Appl	US-09-900-766-7						
131	112.5	9.1	89	17	US-10-767-687-23	Sequence 23, Appl	; Sequence 7, Application US/09900766						
132	110.5	8.9	444	18	US-10-724-972A-4705	Sequence 4705, App	; Publication No. US20030039655A1						
133	109	8.8	232	16	US-10-428-817A-194	Sequence 18, Appl	; GENERAL INFORMATION:						
134	107.5	8.7	234	9	US-09-870-759-18	Sequence 18, Appl	; APPLICANT: FORSBERG, GORAN						
135	107.5	8.7	234	10	US-10-267-682-111	Sequence 11, App	; APPLICANT: ERLANDSSON, EVA						
136	107.5	8.7	234	15	US-10-267-682-111	Sequence 11, App	; APPLICANT: ANTONSSON, PER						
137	107.5	8.7	234	16	US-10-428-817A-14	Sequence 14, Appl	; APPLICANT: WALSE, BJORN						
138	107.5	8.7	234	16	US-10-428-817A-14	Sequence 14, Appl	; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY						
139	107.5	8.7	234	17	US-10-428-817A-189	Sequence 189, App	; FILE REFERENCE: P02188U0;10104199						
140	107.5	8.7	234	16	US-10-937-758A-18	Sequence 18, Appl	; CURRENT APPLICATION NUMBER: US/09/900,766						
141	105.5	8.5	89	14	US-10-002-784A-36	Sequence 36, Appl	; CURRENT FILING DATE: 2001-07-06						
142	105.5	8.5	89	17	US-10-002-784A-36	Sequence 36, Appl	; NUMBER OF SEQ ID NOS: 7						
143	105.5	8.5	89	17	US-10-767-687-21	Sequence 21, Appl	; SOFTWARE: PatentIn version 3.0						
144	105.5	8.5	89	17	US-10-767-687-21	Sequence 21, Appl	; SEQ ID NO 7						
145	105.5	8.5	194	10	US-09-465-714-3	Sequence 3, Appli	; LENGTH: 233						
146	105.5	8.5	194	15	US-10-354-948-6	Sequence 6, Appli	; TYPE: PRT						
147	105.5	8.5	194	16	US-10-763-362-45	Sequence 45, Appl	; ORGANISM: Staphylococcus sp.						
148	105.5	8.5	234	15	US-10-282-122A-70390	Sequence 70390, A	US-09-900-766-7						
149	105.5	8.5	238	10	US-09-465-714-1	Sequence 1, Appli	Query Match 100.0%; Score 1238; DB 10; Length 233;						
150	105	8.5	226	9	US-09-815-242-5900	Sequence 5900, Ap	Best Local Similarity 100.0%; Pred. No. 6.7e-105;						
151	105	8.5	226	9	US-09-815-242-13156	Sequence 13156, A	Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;						
152	104.5	8.4	234	14	US-10-002-784A-12	Sequence 12, Appl							
153	104.5	8.4	234	17	US-10-767-687-12	Sequence 12, Appl							
154	102	8.2	259	16	US-10-425-115-248736	Sequence 248736, A							
155	101	8.2	232	15	US-10-282-122A-70241	Sequence 70241, A							
156	99.5	8.0	231	15	US-10-282-122A-70240	Sequence 70240, A							
157	98.5	8.0	621	15	US-10-424-599-264720	Sequence 264720, A							
158	98.5	8.0	628	15	US-10-425-114-57792	Sequence 57792, A							

QY 1 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMTGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMTGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233

RESULT 2
US-10-283-838-8
; Sequence 8, Application US/10283838
; Publication No. US20030092894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/595,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 8:

US-10-283-838-8
Query Match 100.0%; Score 1238; DB 14; Length 233;
Best Local Similarity 100.0%; Pred. No. 6.7e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 1 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60

QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMTGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGTGNKTACMTGGVTLHDNNRLT 120
QY 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTPVIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENHLIDLTYTT 233

RESULT 3
US-10-267-682-112
; Sequence 112, Application US/10267682
; Publication No. US2004003235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 112:

US-10-267-682-112
Query Match 100.0%; Score 1238; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.6e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLKKSELOLNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84

QY	61	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQACGGTPNKTCACMGVTLHDNNRLT	120
Db	85	HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYYGQACGGTPNKTCACMGVTLHDNNRLT	144
QY	121	EEKKYPINLWIDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLVNSDSFGKQV	180
Db	145	EEKKYPINLWIDGKQTTVPIDKVKTSKEVTVQELDLOARHYLHGKFGLVNSDSFGKQV	204
QY	181	RLGLVPHSGSEGTSVSYDLFDAGQGPDTLLRIYEDNKNTINSENLHIDLVLTT	233
Db	205	RLGLVPHSGSEGTSVSYDLFDAGQGPDTLLRIYEDNKNTINSENLHIDLVLTT	257

RESULT. T. A

```

RESOLUTION 4
US-10-267-748-112
; Sequence 112, Application US/10267748
; Publication No. US20040052820A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION:
; COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV

```

```

Query Match      100.0%; Score 1238; DB 15; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.6e-105;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 SEKSEEINEXDLRKKEQLQNALSNLRQIYYINEKAITENKESDDQFLENTLLPKGFYTG 60
|||||

```

Db	25	SEKSEINEKDKKSEIQRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG	84
Qy	61	HPWYNDLLVDLGSKDATNKYIGKKVDLYGAYYGQCAGTGNKTCMYGGVTLHDNNRLT	120
Db	85	HPWYNDLLVDLGSKDATNKYIGKKVDLYGAYYGQCAGTGNKTCMYGGVTLHDNNRLT	144
Qy	121	EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ	180
Db	145	EKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ	204
Qy	181	RGLVPHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSNLHIDLVLVTT	233
Db	205	RGLVPHSSEGSTVSVDLFDAGQGYPDTLRIYRDNKTINSNLHIDLVLVTT	257

DEC 11 1966

```

RESULT 5
US-10-428-817A-188
; Sequence 188, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 188
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-188

```

```
Query Match      100.0%; Score 1238; DB 16; Length 257;
Best Local Similarity 100.0%; Pred. No. 7.6e-105;
Matches 233: Conservative 0; Mismatches 0; Indels 0; Gaps 0
```

Qy	1	SEKSEEEINEXDLRKKS	ELQNALSNLRQIYYINEKAITENKESDDQFL	ENTLLFKGFFTG	60
Db	25	SEKSEEEINEXDLRKKS	ELQNALSNLRQIYYINEKAITENKESDDQFL	ENTLLFKGFFTG	84
Qy	61	HPWYNDLLVDLGS	KDATNKYGGKVDLYGAYGYQCAGGT	PNKTACMYGGVYTLHNNRLT	120
Db	85	HPWYNDLLVDLGS	KDATNKYGGKVDLYGAYGYQCAGGT	PNKTACMYGGVYTLHNNRLT	144
Qy	121	EEKKVPINLWIDG	KQTTPVDKVKTSKEVTVQELDLQARHYLHGK	FGLYNSDSFGGKVQ	180
Db	145	EEKKVPINLWIDG	KQTTPVDKVKTSKEVTVQELDLQARHYLHGK	FGLYNSDSFGGKVQ	204
Qy	181	RGLIVPHSS	EGSSTVSYDLFAQQGYPTTLRIYRDNKTINSEN	LHIDLYLYTT	233
Db	205	RGLIVPHSS	EGSSTVSYDLFAQQGYPTTLRIYRDNKTINSEN	LHIDLYLYTT	257

DEC 11 1966

US-09-900-766-3
; Sequence 3, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:

APPLICANT: FORSBERG, GORAN
APPLICANT: ERLANDSSON, EVA
APPLICANT: ANTONSSON, PER
APPLICANT: WALSE, BJORN
TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
FILE REFERENCE: P02188US010104199
CURRENT APPLICATION NUMBER: US/09/900,766
CURRENT FILING DATE: 2001-07-06
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 3
LENGTH: 233
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(233)
OTHER INFORMATION: Chimeric Protein
US-09-900-766-3

Query Match 97.7%; Score 1210; DB 10; Length 233;
Best Local Similarity 97.9%; Pred. No. 2.4e-102;
Matches 228; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSENHLIDLYTT 233

RESULT 7
US-09-870-759-16
Sequence 16, Application US/09870759
Patent No. US20020177551A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 870759
CURRENT APPLICATION NUMBER: US/09/870,759
CURRENT FILING DATE: 2002-01-14
PRIOR APPLICATION NUMBER: US 60/208,128
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 248
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-870-759-16

Query Match 96.0%; Score 1188; DB 9; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSEN 224
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSEN 248

RESULT 8
US-09-751-708A-16
Sequence 16, Application US/09751708A
Publication No. US20030157113A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 751708
CURRENT APPLICATION NUMBER: US/09/751,708A
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: US 60/173,371
PRIOR FILING DATE: 1999-12-28
NUMBER OF SEQ ID NOS: 166
SOFTWARE: PatentIn version 3.1
SEQ ID NO 16
LENGTH: 248
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-751-708A-16

Query Match 96.0%; Score 1188; DB 10; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSEN 224
DB 205 RGLIVFHSSEGSTSVSYDLFDAQGYPTDLLRIYRDNKTINSEN 248

RESULT 9
US-10-428-817A-12
Sequence 12, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686

```
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 12
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-12

Query Match          96.0%; Score 1188; DB 16; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 84

Qy 61 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 248

RESULT 10
US-10-937-758A-16
; Sequence 16, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 16
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-16

Query Match          96.0%; Score 1188; DB 17; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e-100; Indels 0; Gaps 0;
Matches 224; Conservative 0; Mismatches 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 84

Qy 61 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 248

RESULT 11
US-09-900-766-2
```

```
; Sequence 2, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: (1)..(233)
; OTHER INFORMATION: Chimeric Protein
US-09-900-766-2

Query Match          89.4%; Score 1107; DB 10; Length 233;
Best Local Similarity 89.7%; Pred. No. 6.4e-93;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 60
Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYYNKAITENKESDDQFLENTLLFKGFFTG 60

Qy 61 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSKDATNKKYKGVLDLYGAYGYQCAGGTENKTCACMYGGVTLHDNNRLT 120

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 233

RESULT 12
US-09-900-766-1
; Sequence 1, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US0;10104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 672
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: PEPTIDE
; LOCATION: (1)..(672)
; OTHER INFORMATION: Conjugate protein
US-09-900-766-1

Query Match          89.4%; Score 1107; DB 10; Length 672;
Best Local Similarity 89.7%; Pred. No. 2.6e-92;
Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;
```

QY 1 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 236 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 285
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 286 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 345
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 346 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 405
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 233
DB 406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 458
RESULT 13
US-09-900-766-4
; Sequence 4, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104139
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-4

Query Match 82.6%; Score 1023; DB 10; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.1e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 233

RESULT 14
US-283-838-7
; Sequence 7, Application US/10283838
; Publication No. US2003002894A1
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlsten,
; Johan Hansson, Terje Kalland, Lars
; Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor

CITY: Houston
STATE: TX
COUNTRY: USA
ZIP: 77027-9095
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/283,838
FILING DATE: 30-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/695,692
FILING DATE: August 12, 1996
APPLICATION NUMBER: 9601245-5
FILING DATE: March 29, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Krieger, Paul E.
REGISTRATION NUMBER: 25,886
REFERENCE/DOCKET NUMBER: 41986/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-850-0909
TELEFAX: 713-850-0165
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-283-838-7

Query Match 82.6%; Score 1023; DB 14; Length 233;
Best Local Similarity 82.0%; Pred. No. 3.1e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALSNLRIQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVLDGSKDANKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
DB 61 HSWYNDLLVDFDSKDIIVDKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYTT 233

RESULT 15
US-10-267-682-113
; Sequence 113, Application US/10267682
; Publication No. US20040033235A1
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; Matthews, Thomas J.
; Wild, Carl T.
; Barney, Shawn O.
; Lambert, Dennis M.
; Petteway, Stephen R.
; Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds

STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,682
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-682-113

Query Match 82.6%; Score 1023; DB 15; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEENEKDLRKSELQNALSNLRQIYYNKAITENKESDDOFLNTLLKGFPTG 60
Db 25 SEKSEENEKDLRKSELQGTALGNLQIYYNKAITENKESHDDQFLQHTILFKGFPTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQNTVPLETVTNKKNVTVQELDLQARRYLOEKYNLYNSDVFDGKVKQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 16
US-10-267-748-113
Sequence 113, Application US/10267748
Publication No. US20040052820A1
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
Matthews, Thomas J.
Wild, Carl T.
Barney, Shawn O.
Lambert, Dennis M.
Petteway, Stephen R.
Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:

ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/267,748
FILING DATE: 08-Oct-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/484,223A
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-029
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 113:
US-10-267-748-113

Query Match 82.6%; Score 1023; DB 15; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-85;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEENEKDLRKSELQNALSNLRQIYYNKAITENKESDDOFLNTLLKGFPTG 60
Db 25 SEKSEENEKDLRKSELQGTALGNLQIYYNKAITENKESHDDQFLQHTILFKGFPTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
Db 145 EEKVPINLWIDGKQNTVPLETVTNKKNVTVQELDLQARRYLOEKYNLYNSDVFDGKVKQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHLDLYLTS 257

RESULT 17
US-10-354-948-4
Sequence 4, Application US/10354948
Publication No. US20030202962A1
GENERAL INFORMATION:
APPLICANT: Dow, Steve W.
Elmslie, Robyn E.
Potter, Terence A.
TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross & McIntosh
STREET: 1700 Lincoln Street, Suite 3500
CITY: Denver
STATE: Colorado
COUNTRY: U.S.A.

ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/10/354,948
APPLICATION NUMBER: US/10/354,948
FILING DATE: 29-Jan-2003
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/580,806
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Connell, Gary J.
REGISTRATION NUMBER: 32,020
REFERENCE/DOCKET NUMBER: 2879-29-C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-354-948-4

Query Match 82.3%; Score 1019; DB 15; Length 233;
Best Local Similarity 81.9%; Pred. No. 7.1e-85;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 61
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 121
DB 62 SWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 121
QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 181
QY 182 GLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 182 GLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233

RESULT 18
US-09-870-759-8
; Sequence 8, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-870-759-8

Query Match 81.8%; Score 1013; DB 9; Length 257;
Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 19
US-09-751-708A-8
; Sequence 8, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; PRIOR FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-751-708A-8

Query Match 81.8%; Score 1013; DB 10; Length 257;
Best Local Similarity 81.5%; Pred. No. 2.9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLDLYLYTT 257

RESULT 20
US-10-428-817A-4
; Sequence 4, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15

```
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 4
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-4

Query Match      81.8%; Score 1013; DB 16; Length 257;
Best Local Similarity 81.5%; Pred. No. 2,9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLPKGPFPTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESHQDQFLQHTILFKGPFPTN 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKKVTVQELDLQARHYLQEKYNYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 21
US-10-937-758A-8
; Sequence 8, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 8
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-8

Query Match      81.8%; Score 1013; DB 17; Length 257;
Best Local Similarity 81.5%; Pred. No. 2,9e-84;
Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLPKGPFPTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESHQDQFLQHTILFKGPFPTN 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
```

```
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKKVTVQELDLQARHYLQEKYNYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 22
US-10-002-784A-2
; Sequence 2, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 257
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A periplasmic
US-10-002-784A-2

Query Match      80.8%; Score 1000; DB 14; Length 257;
Best Local Similarity 80.7%; Pred. No. 4,4e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESDDQFLNTLLPKGPFPTG 60
Db 25 SEKSEINEKDLRKXSELQNALNLRQIYYNKAITENKESHQDQFQHTILFKGPFPTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIDVKYKGVVLDYGYGYOCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWLDGKQNTVPLETVTKNKKVTVQELDLQARHYLQEKYNYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQYPTDLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQGQSNLTLLRIYRDNKTINSENHIDIYLYTS 257

RESULT 23
US-10-767-687-2
; Sequence 2, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
```

```

; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/10/767,687
;   FILING DATE: 29-Jan-2004
;   CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US/08/882,431B
;   FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
;   NAME: Charles H. Harris
;   REGISTRATION NUMBER: 34,616
;   REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (301) 619-2065
;   TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 257
;   TYPE: Amino Acid
;   STRANDEDNESS: Unknown
;   TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-767-687-2

Query Match      80.8%; Score 1000; DB 17; Length 257;
Best Local Similarity 80.7%; Pred. No. 4.4e-83;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 60
DB 25 SEKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 84
QY 61 HPYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 120
DB 85 HSWYNDLLVRFDSKQNTVPLETKNKKVVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EKKVPINLWIDGKQNTVPLETKNKKVVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLT 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPDTLRLIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKTINSENMMHIDIYLYTS 257

RESULT 24
US-10-002-784A-4
; Sequence 4, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 4
; LENGTH: 233
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: mutant staphylococcal enterotoxin A cytoplasmic
US-10-002-784A-4

Query Match      80.5%; Score 996; DB 14; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.1e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;


```

```

QY 2 EKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 61
QY 62 PWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLTE 121
DB 62 SWYNDLLVRFDSKQNTVPLETKNKKVVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVKQ 181
DB 122 EKKVPINLWIDGKQNTVPLETKNKKVVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLTE 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPDTLRLIYRDNKTINSENHLIDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGYNSNTLLRIYRDNKTINSENMMHIDIYLYTS 233

RESULT 25
US-10-767-687-4
; Sequence 4, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 233
;   TYPE: Amino Acid
;   STRANDEDNESS: Unknown
;   TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-767-687-4

Query Match      80.5%; Score 996; DB 17; Length 233;
Best Local Similarity 80.6%; Pred. No. 9.1e-83;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 61
DB 2 EKSEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDOFLNTLLFKGFTTG 61
QY 62 PWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHNNRLTE 121
```

```
Db 62 SWYNDLLVRPDSKOTVDYKGGKVDLYGAYAGYQCAGGTPNKTCACMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVOR 181
Db 122 EKKVPINLWIDGKQNTVPLETVKTKGNVTVQELDLQARRYLQEKYINLNSDVDFGKVOR 181
Qy 182 GLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 233

RESULT 26
US-10-428-817A-182
; Sequence 182, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 182
; LENGTH: 231
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-182

Query Match 80.0%; Score 991; DB 16; Length 231;
Best Local Similarity 80.3%; Pred. No. 2,6e-82;
Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLPKGPFPTG 60
Db 1 SEKSEINEKDLRKKSSELQGTAA--GNKQIYYNYNEKAKTENKESHQDFLQHTILFKGPFPTD 58
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 59 HSWYNDLLVDFPSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 118
Qy 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 119 EKKVPINLWIDGKQNTVPLETVKTKGNVTVQELDLQARRYLQEKYINLNSDVDFGKVQ 178
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 179 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 231
```

```
RESULT 27
US-08-882-431-2
; Sequence 2, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
```

```
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431-2

Query Match 79.4%; Score 983; DB 8; Length 257;
Best Local Similarity 79.8%; Pred. No. 1.6e-81;
Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLPKGPFPTG 60
Db 25 SEKSEINEKDLRKKSSELQGTALGNLQIYYNYNEKAKTENKESHQDFRQHTILFKGPFPTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFPSKDIVDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
Qy 121 EKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EKKVPINLWIDGKQNTVPLETVKTKGNVTVQELDLQARRYLQEKYINLNSDVDFGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSNMHIDIYLYTS 257

RESULT 28
US-08-882-431-4
; Sequence 4, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
```

CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 233
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-4

Query Match 79.0%; Score 978; DB 8; Length 233;
Best Local Similarity 79.3%; Pred. No. 4e-81;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOALNSLRQIYYNYNEKAITENKESDDQPLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESHDQPROHTILFKGFFTDH 61
QY 62 PWNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
DB 122 EKKVPINLWDGKQTTVPLETVTKNKNVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRDNKTINSENHIDIYLYTS 233

RESULT 29
US-10-997-690-11
Sequence 11, Application US/10997690
Publication No. US20050153376A1
GENERAL INFORMATION:
APPLICANT: FRASER, JOHN DAVID
APPLICANT: PROFT, THOMAS
TITLE OF INVENTION: SUPERNANTIGENS
FILE REFERENCE: 12669-004001
CURRENT APPLICATION NUMBER: US/10/997,690
CURRENT FILING DATE: 2004-11-24
PRIOR APPLICATION NUMBER: 09/869,136
PRIOR FILING DATE: 2001-07-20
PRIOR APPLICATION NUMBER: PCT/NZ99/00228
PRIOR FILING DATE: 1999-12-24
PRIOR APPLICATION NUMBER: NZ 333589
PRIOR FILING DATE: 1998-12-24
NUMBER OF SEQ ID NOS: 25
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11

LENGTH: 227
TYPE: PRT
ORGANISM: Streptococcus aureus
US-10-997-690-11

Query Match 74.4%; Score 921; DB 18; Length 227;
Best Local Similarity 79.4%; Pred. No. 6.3e-76;
Matches 185; Conservative 17; Mismatches 25; Indels 6; Gaps 6;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELOALNSLRQIYYNYNEKAITENKESHDQFLQHTILFKGFFTN 59
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLT 120
DB 60 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTAACMY-GVTLHDNNRLT 118
QY 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 119 BEKKVPINLWDG-KQNTVPLETVTKNKNVTVOELDLQAR-YLQEKYNL-NSDVFQKQV 175
QY 181 RGLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLIDLYLYTT 233
DB 176 RGLIVFHTSTEPSVNYDLFGAQGQYNTLLRIYRD-KTINSENHIDIYLYTS 227

RESULT 30
US-10-428-817A-175
Sequence 175, Application US/10428817A
Publication No. US20040214783A1
GENERAL INFORMATION:
APPLICANT: TERMAN, David S
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: 38373-189118
CURRENT APPLICATION NUMBER: US/10/428,817A
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: US 60/378,988
PRIOR FILING DATE: 2002-05-08
PRIOR APPLICATION NUMBER: US 60/389,366
PRIOR FILING DATE: 2002-06-15
PRIOR APPLICATION NUMBER: US 60/406,697
PRIOR FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: US 60/406,750
PRIOR FILING DATE: 2002-08-29
PRIOR APPLICATION NUMBER: US 60/415,310
PRIOR FILING DATE: 2002-10-01
PRIOR APPLICATION NUMBER: US 60/415,400
PRIOR FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: US 60/438,686
PRIOR FILING DATE: 2003-01-09
NUMBER OF SEQ ID NOS: 224
SOFTWARE: PatentIn version 3.2
SEQ ID NO 175
LENGTH: 268
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-10-428-817A-175

Query Match 67.0%; Score 830; DB 16; Length 268;
Best Local Similarity 64.9%; Pred. No. 1.7e-67;
Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

QY 3 KSEINEKDLRKSELOALNSLRQIYYNYNEKAITENKESDDQPLENTLLFKGFFTGHP 62
DB 27 KNETIKEKNLHKSELSITLNNLRHIYFNEKISEKIMTEQDFLDYTLFPKSFISHS 86
QY 63 WYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNRLTEE 122
DB 87 QYNDLLVDFDSKETVKNKFGKVDLYGAYGYQCAGGTPNKTAACMYGGVTLHDNNLYDT 146
QY 123 KKVPIINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 182
DB 147 KKVPIINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVOR 206


```

; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 187
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; US-10-428-817A-187

```

Query Match	53.6%	Score 663	DB 16	Length 258
Best Local Similarity	54.5%	Pred. No. 3e-52		
Matches 126	Conservative	35	Mismatches 70	Indels 0
Gaps 0				
Qy	1	SEKSEETNEVDLRKXSELQNALSNLRQIYYVNEKAITENKESDDQFLENTLLAFKGFPTG	60	
Db	26	NEMIDSVKELHKKSELSTALNNMKHSYADKNPPIGENKSTGDQFLENTLLYKKFFTD	85	
Qy	61	HPWYNDDLVLGSKDANTYKVGKKVDLYGAYGYQCAGTTPNKTACMYGGVTLHNNRLT	120	
Db	86	LINPEDLLINFNSKEMAHFKSKNDVVPYRISYNCYGGEIDRTACTYGGVTPHEGNK	145	
Qy	121	BEKKVPINLWIDGQTTPVDIKVTSKKEVTVQELDLQARHYLHGKFLYNSDFSFGKVQ	180	
Db	146	ERKKIPINLWINGQKVEVSLDKVTDKKNVTVQELDLQARRYLQKDLKLYNNDTLGGKIQ	205	
Qy	181	RGLTIVHSSSEGSTVSYDLFDAQQGYPTDLLIYRDNKTINTSENLIHDIPLY	231	
Db	206	RGKTEPSSDGSKYSYDLFDVKGFPPPEKOLFIYSDNKTLSPEHLIHDIPLY	256	

```

RESULT 35
US-10-937-758A-14
; Sequence 14, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-937-758A-14

```

Query Match 53.6%; Score 663; DB 17; Length 258;
Best Local Similarity 54.5%; Pred. No. 3e-52;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;
Ov 1 SEKSEINEKDLRKKEIQNALNSLRIYYNEKAITENKESDDQFLENTLLPKGPTG 60

26	NENIDS	VKE	KEL	H	K	S	E	L	S	T	A	L	N	M	K	H	S	Y	A	D	K	P	I	G	E	N	K	S	T	G	D	Q	F	L	E	N	T	L	L	Y	K	F	F	T	D	85										
61	HPW	N	D	L	L	V	D	L	G	S	D	A	T	N	K	Y	K	G	K	V	D	L	Y	G	A	Y	G	Y	Q	C	A	G	T	P	N	K	T	A	C	M	Y	G	G	V	T	L	H	D	N	N	R	U	T	120		
86	L	I	N	F	E	D	L	L	I	N	F	N	S	K	E	M	A	H	P	K	S	K	N	V	D	V	P	I	R	S	I	N	C	Y	G	B	I	D	R	T	A	C	T	Y	G	G	V	T	P	H	E	G	N	K	L	145
121	B	E	K	V	P	I	N	L	M	I	D	G	O	T	T	V	P	D	I	K	V	T	S	K	E	V	T	V	Q	E	L	D	L	O	A	R	H	L	H	G	F	G	L	I	N	S	D	S	F	G	G	K	V	180		
146	E	R	K	K	I	P	I	N	L	M	I	N	G	V	Q	E	S	L	D	K	V	T	D	K	N	V	T	V	Q	E	L	D	A	A	R	Y	L	Q	K	D	L	K	L	N	N	D	T	L	G	G	K	I	Q	205		
181	R	G	L	I	V	F	H	S	S	E	G	S	T	S	Y	L	D	F	A	Q	G	Y	P	O	T	L	L	I	R	I	R	D	N	K	T	I	N	S	E	N	L	H	I	D	I	V	L	Y	231							
206	R	G	K	T	E	F	S	D	G	S	K	Y	S	D	L	F	D	V	K	G	P	P	E	K	O	L	A	R	I	S	D	N	K	T	L	S	T	E	H	L	H	I	D	I	V	L	Y	256								

```

RESULT 36
US-09-900-766-5
; Sequence 5, Application US/09900766
; Publication No. US20030039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188US010104199
; CURRENT APPLICATION NUMBER: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 203
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-5

```

	Query Match	42.2%	Score 523;	DB 10;	Length 203;
	Best Local Similarity	49.5%;	Pred. No. 1.4e-39;		
	Matches 109;	Conservative	25;	Mismatches 66;	Indels 20; Gaps 3;
Qy	12	LRKXSELQRLNLSRLQIYYNYNEKAIYENKESDDQFLENTILLPKGFFTGHPWYNDLLVLDL	71		
Db	2	LHKXSELSSLTANNNKHSYADANPIIGANKSTGQFLENTILLYKAF-----LLINF	53		
Qy	72	GSKDATNKYKKGVLDLYGAYYGYOCAGTGNKTCMTGGVTLHNNRLTEBKVPINLWI	131		
Db	54	NSAEMAHFKSKNVDVYAIRYAAAC-----RTACTYGGVTPHAGNALKARKKIPINLWI	107		
Qy	132	DGKOTTPVIDKVKTSKKEVTVOEILDQARHYLHGKFLGINSDSFGGKVQRGILVVFHSEG	191		
Db	108	IGVQKVELSKQVTDKNVTVQEILDQAQRYLQKDLKLYNA-----IQRGKLEFDSAAA	161		
Qy	192	STVSYDLFDAQGYPDTLRLRIYRDNKNTINSENHLIDLYL	231		
Db	162	SKVSYDLFDAQGEPEKOLRIYSNNKTLSTELHLIDLYL	201		

```

RESULT 37
US-10-002-784A-34
; Sequence 34, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
;
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-08-23; 98-09-01
; NUMBER OF SEQ IDS NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0

```

```
; SEQ ID NO 34
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin E
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-34

Query Match          36.9%; Score 457; DB 14; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 0;

Qy 43 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
Db 1 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 38
US-10-767-687-19
; Sequence 19, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/POCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19

Query Match          36.9%; Score 457; DB 17; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 0;

Qy 43 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
```

```
Db 1 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 39
US-10-002-784A-32
; Sequence 32, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 32
; LENGTH: 82
; TYPE: PRT
; ORGANISM: staphylococcal enterotoxin A
; FEATURE:
; OTHER INFORMATION: partial sequence as shown in Figure 3
US-10-002-784A-32

Query Match          32.2%; Score 399; DB 14; Length 82;
Best Local Similarity 86.6%; Pred. No. 9.2e-29;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

Qy 43 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
Db 1 SHDQFLQHTILFKGFFTDHWSYNDDLVDVDFSDKIDVDKYKGKKVDLYGAYGYQCAGGTPN 60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 40
US-10-767-687-17
; Sequence 17, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/POCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-10-767-687-19

Query Match          36.9%; Score 457; DB 17; Length 82;
Best Local Similarity 100.0%; Pred. No. 4.6e-34; Indels 0; Gaps 0;
Matches 82; Conservative 0; Mismatches 0;

Qy 43 SDDQFLENTLLFKGFFTGHPWYNDDLVDLGSKDATNKYKGKKVDLYGAYGYQCAGGTPN 102
```



```

; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-10-767-687-17

Query Match      32.2%; Score 399; DB 17; Length 82;
Best Local Similarity 86.6%; Pred. No. 9.2e-29;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;

QY 43 SDQFLENTLLPKGFTGHPWNLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTN 102
Db 1 SHDQFLQHTILPKGFTDHSWYNDLLVDFDPSKDIDVKYKGGKVDLYGAYGYQCAGGTN 60

QY 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 41
US-09-900-766-6
; Sequence 6, Application US/09900766
; Publication No. US2003039655A1
; GENERAL INFORMATION:
; APPLICANT: FORSBERG, GORAN
; APPLICANT: ERLANDSSON, EVA
; APPLICANT: ANTONSSON, PER
; APPLICANT: WALSE, BJORN
; TITLE OF INVENTION: A NOVEL ENGINEERED SUPERANTIGEN FOR HUMAN THERAPY
; FILE REFERENCE: P02188U0;10104199
; CURRENT FILING DATE: US/09/900,766
; CURRENT FILING DATE: 2001-07-06
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus sp.
US-09-900-766-6

Query Match      29.6%; Score 366; DB 10; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.4e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELRNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFTGHPWNLLV 69
Db 1 EDLHDKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 56 KPATADLAQKFKNKVNDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114

QY 130 WIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVGRLIVFHSS 189
Db 115 WVDGIQKETEL--IRTNKGNVTQLQELDIKIRKILSDKYKIYKDS---BISKGLIEFDMK 169

QY 190 EGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENH-HIDLILYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSKDDISHIDVNLTYT 213

RESULT 42
US-10-428-817A-173
; Sequence 173, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT FILING DATE: 2003-05-05
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 173
; LENGTH: 217
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-428-817A-173

Query Match      29.6%; Score 366; DB 16; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.4e-25;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELRNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFTGHPWNLLV 69
Db 1 EDLHDKSELTDLALAN--AYQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55

QY 70 DLGSKDATNKYKGGKVDLYGAYGYQCAGGTNKTACMYGGVTLHDNNRLTEKKVPINL 129
Db 56 KPATADLAQKFKNKVNDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114

QY 130 WIDGKQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGLYNSDSFGKVGRLIVFHSS 189
Db 115 WVDGIQKETEL--IRTNKGNVTQLQELDIKIRKILSDKYKIYKDS---BISKGLIEFDMK 169

QY 190 EGSTVSVDLFDAGQGPDTLLRIYRDNKTINSENH-HIDLILYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSKDDISHIDVNLTYT 213

RESULT 43
US-10-474-792-416
; Sequence 416, Application US/10474792
; Publication No. US20040236072A1
; GENERAL INFORMATION:
; APPLICANT: Olmsted, Stephen
; APPLICANT: Zagursky, Robert
; APPLICANT: Nickbarg, Elliot
; APPLICANT: Winter, Lourie
; TITLE OF INVENTION: SURFACE PROTEINS OF STREPTOCOCCUS PYOGENES
; FILE REFERENCE: AM 100399
; CURRENT FILING DATE: 2003-10-14
; CURRENT FILING DATE: 2003-10-14
; NUMBER OF SEQ ID NOS: 674
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 416
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-474-792-416
```



```
Qy 2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTAQMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
```

RESULT 55

```
US-09-150-947B-12
; Sequence 12, Application US/09150947B
; Patent No. US20020028211A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM PYROGENIC EXOTOXINS
; TITLE OF INVENTION: ANTAGONISTS AND VACCINES
; FILE REFERENCE: A31967-PCT-USA-A
; CURRENT APPLICATION NUMBER: US/09/150,947B
; CURRENT FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-150-947B-12
```

```
Query Match 24.2%; Score 299.5; DB 9; Length 239;
Best Local Similarity 33.7%; Pred. No. 4.7e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
```

```
Qy 2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTAQMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
```

RESULT 56

US-10-172-425B-12

```
; Sequence 12, Application US/10172425B
; Publication No. US20030147908A1
; GENERAL INFORMATION:
; APPLICANT: Kaempfer, Raymond
; APPLICANT: Arad, Gila
; TITLE OF INVENTION: BROAD SPECTRUM ANTAGONISTS AND VACCINES
; TITLE OF INVENTION: DIRECTED AGAINST PYROGENIC EXOTOXINS
; FILE REFERENCE: A31967-PCT-USA-A-A 066031.0164
; CURRENT APPLICATION NUMBER: US/10/172,425B
; CURRENT FILING DATE: 2002-06-13
; PRIOR APPLICATION NUMBER: 09/150,947
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: PCT/IL97/00438
; PRIOR FILING DATE: 1997-12-30
; PRIOR APPLICATION NUMBER: ISRAEL 119938
; PRIOR FILING DATE: 1996-12-30
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-172-425B-12
```

```
Query Match 24.2%; Score 299.5; DB 14; Length 239;
Best Local Similarity 33.7%; Pred. No. 4.7e-19;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
Qy 2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFFTGH 61
Db 1 ESQDPKPDELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTAQMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRTKCTMYGGV 118
Qy 112 TLHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTAAQELDYLRHYLVKNKKLYE 176
Qy 172 SDSFGGKVQRLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNKNMVDSDKVIEVY 233
Qy 230 LYT 232
Db 234 LTT 236
```

RESULT 57

```
US-10-428-817A-163
; Sequence 163, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
```

Query Match	23.8%	Score	294.5;	DB	8;	Length	251;	
Best Local Similarity	34.2%	Pred. No.	1.4e-18;					
Matches	81;	Conservative	45;	Mismatches	92;	Indels	19; Gaps	10;
Qy	4	SEETNEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT--ENKESDDQFLENTLLFKGFFTG	60					
Dd	25	SQEVFAQQDPPSLHRSSLVKNLQNIYFLYEGDPVTHENVKSDQLLSHLLIYN--VS	81					
Qy	61	HPWYNDLLVLGSKDATNKYGKKVDLYGAYGVQC-AGGTPNKTCAMGYGVTLHDNNRL	119					
Dd	82	GPNTDKLKTELNGOEMATLFKDKNQDIYGVSYHYLCYLCEAERSACTYGGVTWHEGNHL	141					
Qy	120	TEEKVPINLWDGQTTPIDVKVTSKEVTVQELDLPQAARHLYHGKFGLYNSDSFGGKV	179					
Dd	142	EIPKIVVKVSGIDGIQ-SLSFD-IETNKQWTAQELDYKVRKYLTDNKQLYTNGP--SKY	197					
Qy	180	QRGLIVFHSSRGSTVSYDLFD----AQGYPDITLLRIYRDNKTINSENMLHIDLIIYT	232					
Dd	198	ETGYIKFTPKPNKESFWFFPEPPTQSKY---LMYKDNETLDNSTSQIEVLVTT	250					

RESULT 60

Query Match 23.7%; Score 293.5; DB 14; Length 266;
Best Local Similarity 32.8%; Pred. No. 1.9e-18;

Query Match	23.7%	Score 293.5;	DB 17;	Length 266;
Best Local Similarity	32.8%;	Pred. NO. 1.9e-18;		
Matches 80: Conservative	45;	Mismatches 100;	Indels 19;	Gaps 7


```
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 16
; LENGTH: 251
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: streptococcal pyrogenic exotoxin-A mutant
US-10-002-784A-16

Query Match      23.4%; Score 289.5; DB 14; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.1e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy      4 SEEINEKDLRKSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db      25 SOEVAQDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VS 81
Qy      61 HPWNDDLVLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGVTLHDNNRL 119
Db      82 GPNYDKLKTTELKQEMATLFKDKNVDIYGVVEYHLCYLCEAERSACTIYGGVTNHEG NHL 141
Qy      120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db      142 EIPKKIVVKSIDGIQ-SLSFD-IETNKKMWTAQELDYKVRKYLTDNKQLYTNGP--SKY 197

Qy      180 QRGLIVFHSSEGSTVSYDLFD---AQQYPTDLLRIYRDNKTINSENHLIDLYLT 232
Db      198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVILTT 250

RESULT 66
US-10-767-687-16
; Sequence 16, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;           Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRCM -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
```

```
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-767-687-16

Query Match      23.4%; Score 289.5; DB 17; Length 251;
Best Local Similarity 33.8%; Pred. No. 4.1e-18;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy      4 SEEINEKDLRKSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
Db      25 SOEVAQDDPDSQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN---VS 81
Qy      61 HPWNDDLVLGSKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGVTLHDNNRL 119
Db      82 GPNYDKLKTTELKQEMATLFKDKNVDIYGVVEYHLCYLCEAERSACTIYGGVTNHEG NHL 141
Qy      120 TEEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 179
Db      142 EIPKKIVVKSIDGIQ-SLSFD-IETNKKMWTAQELDYKVRKYLTDNKQLYTNGP--SKY 197

Qy      180 QRGLIVFHSSEGSTVSYDLFD---AQQYPTDLLRIYRDNKTINSENHLIDLYLT 232
Db      198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVILTT 250

RESULT 67
US-10-002-784A-10
; Sequence 10, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
; /33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; CURRENT FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 10
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURES:
; OTHER INFORMATION: mutant staphylococcal enterotoxin B cytoplasmic
US-10-002-784A-10

Query Match      23.3%; Score 288.5; DB 14; Length 239;
Best Local Similarity 33.9%; Pred. No. 4.8e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy      14 KKSELRQNA-----LSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
Db      7 KPDELHKSSKFTGLMNNKLVLDNHNVSAT-NVKSIDQFRYFDLYISIKDTKLGNDNVR 65
Qy      69 VDLGSKDATNKYKGVLDLYGAYGYQCAGG-----TPNKTACMYGVTLHDNNR 118
Db      66 VEFKNKDLADKYDKYVDVFGANNAYQCAFSKKTNDINSHQTDKRTKTCMYGVTEHNGNQ 125
Qy      119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKV 178
Db      126 LDKYRSITVRVFEDGK-NLLSFD-VQTNKKKVTQAQELDYLRHYLVKNKKLYEFNN--SP 181
Qy      179 VQRGLIVFHSSEGSTVSYDLFDAGQGYPD--TLARIYRDNKTINSENHLIDLYLT 232
Db      182 YETGYIKFIENENS-FWYDMMPAGDFDOSKYLMMYNDNKNQVDSKOVKIEVILTT 236
```

```

; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Behach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-3

Query Match      23.3%; Score 288.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 4.8e-18;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKESLQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLPKGFPTGHPWYNDLLV 69
DB 10 DLKSEF-TGTMGNMK--YLDHVDHVSATKVKSDVKFLAHLIYINISDKKLKNDYDKVT 66
QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLAKKYKDEVDVYGSNYNCYPSSKDNVGVKTGGKTCMYGGITKEGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVRVY-ENKRTISFE-VQTDKKSVAQAELDIKARNLINKKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 183 TGYIKFIENNGNTFOYDMMAPGDFKQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 70
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:

; Publication No. US10767687
; Sequence 10, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street MCMR-JA (Charles H. Harris-Patent A
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/767,687
; FILING DATE: 29-Jan-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:

US-10-767-687-10

Query Match      23.3%; Score 288.5; DB 17; Length 239;
Best Local Similarity 33.9%; Pred. No. 4.8e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

QY 14 KKSELQNA-----LSNLRLQIYYNEKAITENKESDDQFLENTLLPKGFPTGHPWYNDLL 68
DB 7 KPDELHKSSKFTGLMENMKVLYDDNHVSAI-NVKSIDQFRYFDLYISIKDTKLGNVDNR 65
QY 69 VDLGSKDATNKYKGVLDLYGAYGYQCAGG-----TPNKTACMYGGVTLHDNR 118
DB 66 VEPFNKDLADKYKDYVDVFGANAYYQCAFSKKTNDINSHQTDKRTCMYGGVTEHNGNQ 125
QY 119 LTEEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGK 178
DB 126 LDKRSITVRVFDGK-NLLSFD-VQTNKKKVAQAELDYLRHYLVKNKKLYEFNN--SP 181
QY 179 VQRGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 182 YETGYIKFIENENS-FWYDMMAPGDFKQSKYLMYNDNKNKVDKSVKIEVHLTT 236

RESULT 69
US-10-923-324-3
; Sequence 3, Application US/10923324
```

```

; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Behach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USMO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 3
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-3

Query Match      23.3%; Score 288.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 4.8e-18;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLKESLQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLPKGFPTGHPWYNDLLV 69
DB 10 DLKSEF-TGTMGNMK--YLDHVDHVSATKVKSDVKFLAHLIYINISDKKLKNDYDKVT 66
QY 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122
DB 67 ELLNEDLAKKYKDEVDVYGSNYNCYPSSKDNVGVKTGGKTCMYGGITKEGHNFDNG 126
QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 127 NLQNLVRVY-ENKRTISFE-VQTDKKSVAQAELDIKARNLINKKNLYEFNS--SPYE 182
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLXYLT 232
DB 183 TGYIKFIENNGNTFOYDMMAPGDFKQSKYLMYNDNKTVDKSVKIEVHLTT 236

RESULT 70
US-08-882-431-10
; Sequence 10, Application US/08882431
; Publication No. US2003009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MPMC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431-10

Query Match 23.2%; Score 287.5; DB 8; Length 239;
Best Local Similarity 33.9%; Pred. No. 5.9e-18;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KKSEIQRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLL 68
Db 7 KPDELHKSSKSTGKWMKNKLYDDNHVSAI-NVKSIDQFRYFDLIYSIKDTKLGNYDNVR 65

Qy 69 VDLGSKDATNKYKGGKVDLYGAYGYQCAGG-----TPNKTACMYGGVTLHNNR 118
Db 66 VEFKNKDLADKYKDYVDFGANAYYQCAFSSKTKTNDINSHQTDKRTKTCMYGGVTEHNGQ 125

Qy 119 LTEBKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGK 178
Db 126 LDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDLTRHYLVKDKKLYEFNN--SP 181

Qy 179 VQGLIVPHSSEGSTVSVDLFDQAQGYPD--TLRLIYRDNKTINSENLHIDLYLT 232
Db 182 YETGVKIEIENS-FWDDMPAPGDKFDQSKYLMYNDNKWDSKDVKIEVLT 236

RESULT 71
US-10-923-324-6
; Sequence 6, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-6

Query Match 23.2%; Score 287.5; DB 17; Length 240;
Best Local Similarity 32.1%; Pred. No. 5.9e-18;
Matches 75; Conservative 48; Mismatches 92; Indels 19; Gaps 9;

Qy 11 DLKKSEIQRNA--LSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTGHPWYNDLLV 69
```

```
Db 10 DLHKSSSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHDLIYINISDKLKNYDKVKT 66
Qy 70 DLGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTLHNNRLTEE 122
Db 67 ELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITTKHEGNHFDNG 126
Qy 123 --KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 127 NLQNVLRVY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYEFNS--SPYE 182
Qy 181 RGLIVPHSSEGSTVSVDLFDQAQGYPD--TLRLIYRDNKTINSENLHIDLYLT 232
Db 183 TGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVHLT 236

RESULT 72
US-10-923-324-5
; Sequence 5, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (240)..(240)
; OTHER INFORMATION: Xaa is unknown.
US-10-923-324-5

Query Match 23.1%; Score 285.5; DB 17; Length 240;
Best Local Similarity 31.3%; Pred. No. 9e-18;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

Qy 2 EKSEINEKDLKKSEIQRNA--LSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
Db 1 ESQPDPTPDELHKSSSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHDLIYINISDKK 57
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKTACMYGGVTL 113
Db 58 LKNYDKVKTELLNEDLAKYKDEVDVYGSNYVNCYFSSKDNVKGVTGGKTCMYGGITK 117
Qy 114 HDNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFDNGNLQNLVIRY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKKNLYE 175
Qy 172 SDSFGKVGQRLIVFHSSEGSTVSVDLFDQAQGYPD--TLRLIYRDNKTINSENLHIDLY 229
Db 176 FNS--SPYETGYIKFTIENNGNTFOYDMMPPAPGDKFDQSKYLMYNDNKTVDSKRVKIEVH 233
Qy 230 LYT 232
Db 234 LTT 236
```

```
RESULT 73
US-10-428-817A-186
; Sequence 186, Application US/10428817A
; Publication No. US20040214783A1
```

```

RESULT 74
US-10-923-324-2
; Sequence 2, Application US/10923324
; Publication No. US20050026272A1
; GENERAL INFORMATION:
; APPLICANT: Bohach, Gregory I.
; TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
; FILE REFERENCE: 12136.1USWO
; CURRENT APPLICATION NUMBER: US/10/923,324
; CURRENT FILING DATE: 2004-08-20
; PRIOR APPLICATION NUMBER: US/09/555,115
; PRIOR FILING DATE: 2000-08-01
; PRIOR APPLICATION NUMBER: PCT/US98/25107
; PRIOR FILING DATE: 1998-12-01
; PRIOR APPLICATION NUMBER: US 60/067,357
; PRIOR FILING DATE: 1997-12-02
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: ERT
; ORGANISM: Staphylococcus aureus
; FEATURE:
; NAME/KEY: MISC FEATURE

```

	Query Match	22.8%	Score 282.5;	DB 14;	Length 266;	
	Best Local Similarity	32.8%;	Pred. No. 1.9e-17;			
	Matches	80; Conservative	46; Mismatches	99; Indels	19; Gaps	8
Qy	1 SEKSEETNEKDLRRKKSELQRNALSNLRQIYYVYNEKAITENKESDDQLFLENTLLFKGFFTG	60	:	:	:	:
Dd	27 AESQPDKPDELHKSSKF-TGLMENMKVLVDNDHVSAL-NVKSIDQPRFYDFLIIYSIKDTH	84	:	:	:	:
Qy	61 HPWTNDDLVLGSKDATNKYGKKVDLYGAYGYOCAGG-----TENKTACMYGG	110	:	:	:	:
Dd	85 LGNYDNVRVEFNKLADKYDKDYGVFGANWAYVCAPSKTKTINDINSHOTDKRTCTMTGG	144	:	:	:	:
Qy	111 VTLHDNNRLTEEEKVPINLMWIDGRQTTPVIDKVTSKEEVTQVELDQARHYLHGKGFLY	170	:	:	:	:
Dd	145 VTEHNGNQLDKYSITVRVPEDGK-NLLSPD-VQYNKKKVTAQELDYLTRHYLVKNKKLY	202	:	:	:	:
Qy	171 NSDSFGKGVBQCLIVFHSSSEGSTVSYDLFDAQQOYPD--TLLRLYRDNKTNTENSENLHTDL	228	:	:	:	:
Dd	203 EFNK--GPYETGYIAKFIEENENS-FWYDMMPAPGDGFQSDKTYLMMYNDNRNVDSKDVLEV	259	:	:	:	:
Qy	229 YLYT	232	:	:	:	:

[illegible]

STREET: US Army MRC -504 Scott Street MCMR-JA (John Moran-Patent Atty)
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Moran, John
REGISTRATION NUMBER: 26,313
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 265
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
US-08-882-431-6

Query Match 22.6%; Score 280; DB 8; Length 265;
Best Local Similarity 31.6%; Pred. No. 3.3e-17;
Matches 77; Conservative 45; Mismatches 102; Indels 20; Gaps 7;
QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYVYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 27 ASQPPKPEDELHKSKEF--TGLMEDMKVLYDDNHVSAINVKSIDQFLFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQC-----AGGTPNKTKACMYGG 110
DB 85 LGDYDNVRVEFKNKDLADKYKVDVFGVYNYCYFYFSKKTNDINSHQTKRKTCTMYG 144
QY 111 VTLHDNNRLTEEEKVPIWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLY 170
DB 145 VTEHNGNQLDKYRSITVRVFDGK--NLLGPD--VOYNKKKVTQAQELDYLTRHYLVKNKKLY 202
QY 171 NSDSFGKVQVGLIVFHSSEGSTVSYDLFDAQGQ--YPTDLLRIYRDNKTINSNLHIDL 228
DB 203 EFN--SPYETGYIKF--TENQNFWDMPAPGDKFAQSKYLMYNDNKNVDSKDVKLEV 258
QY 229 YLYT 232
DB 259 YLTT 262

RESULT 79
US-10-923-324-7
Sequence 7, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US/09/555,115
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357

PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in version 3.1
SEQ ID NO 7
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-10-923-324-7

Query Match 22.3%; Score 276.5; DB 17; Length 240;
Best Local Similarity 30.5%; Pred. No. 6e-17;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELQNALSNLRQIYYVYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDTPDELHKSKEF--TGLMENMKVL--YDRIYVSATKVKSVDFLAHLDIYINISDKK 57
QY 61 HPWYNDLLVLDGSKDATNKGKVDLYGAYGYQC-----AGGTPNKTKACMYGGVTL 113
DB 58 LKDYDKVTELLNEDLAKYKDEVDVYVGSNYVNCYFSDKNVGVKVTGKTCMYGKITK 117
QY 114 HDNNRLTEE--KKVPIWIDGKQTTVPIDKVKTSKKEVTVQELDQARHYLHGKFLY 171
DB 118 HEGNHFDNGNLQNLIRVY--ENKRNITISPE--VQTDKKSVTQAQELDIKARNFLLINKKNLYE 175
QY 172 SDSFGKVQVGLIVFHSSEGSTVSYDLFDAQGQYD--TLLRIYRDNKTINSNLHIDL 229
DB 176 FNS--SPYETGYIKF--FIENNGNTFYDMMMPAPGDKFDQSKYLMYNDNKTVDKSRVKIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 80
US-10-923-324-8
Sequence 8, Application US/10923324
Publication No. US20050026272A1
GENERAL INFORMATION:
APPLICANT: Bohach, Gregory I.
TITLE OF INVENTION: NON-TOXIC IMMUNE STIMULATING ENTEROTOXIN COMPOSITIONS
FILE REFERENCE: 12136.1USWO
CURRENT APPLICATION NUMBER: US/10/923,324
CURRENT FILING DATE: 2004-08-20
PRIOR APPLICATION NUMBER: US/09/555,115
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: PCT/US98/25107
PRIOR FILING DATE: 1998-12-01
PRIOR APPLICATION NUMBER: US 60/067,357
PRIOR FILING DATE: 1997-12-02
NUMBER OF SEQ ID NOS: 66
SOFTWARE: Patent in version 3.1
SEQ ID NO 8
LENGTH: 240
TYPE: PRT
ORGANISM: Staphylococcus aureus
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (240)..(240)
OTHER INFORMATION: Xaa is unknown.
US-10-923-324-8

Query Match 22.3%; Score 276.5; DB 17; Length 240;
Best Local Similarity 30.5%; Pred. No. 6e-17;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;
QY 2 EKSEINEKDLRKSELQNALSNLRQIYYVYNEKAITENK-ESDDQFLENTLLFKGFFTG 60
DB 1 ESQPDTPDELHKSKEF--TGLMENMKVL--YDRIYVSATKVKSVDFLAHLDIYINISDKK 57

Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYVGYQC-----AGGTENKTCMYGGVTL 113
Db 58 LKNYDKVKVTELLNEDLAKYKDEVDVVGYSYNNCCFFSKDNVGVKVTGGKTCMYGGITK 117
Qy 114 HDNRLTBE--KKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 118 HEGNHFDGNLQNVLRVY-ENKRNtisFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
Qy 172 SDSFGGKVQVGLIYVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDL 229
Db 176 FNS--SPYETGYIKFPIENNGNTFYDMMPPAGDKFDQSKYLMYNDNKTVDSDKRVKIEVH 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 81
US-08-892-431-8
; Sequence 8, Application US/08882431
; Publication No. US20030009015A1
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: John Moran
; STREET: US Army MRC - 504 Scott Street MCMR-JA (John Moran-Patent Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Moran, John
; REGISTRATION NUMBER: 26,313
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 265
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-892-431-8

Query Match 22.3%; Score 276; DB 8; Length 265;
Best Local Similarity 32.0%; Pred. No. 7.6e-17;
Matches 78; Conservative 46; Mismatches 100; Indels 20; Gaps 8;

Qy 1 SEKSEINEKDLRKSELQNALSNLROIYYNNEKAITENKESDDQFLENTLLFKGFFPTG 60
Db 27 AESQDPKPDHLKSGKF-TGLMENMKVLYDDNHVSAT-NVKSIDQFRLIYSIKDTK 84
Qy 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYVGYQCAGS-----TPNKTACMYGG 110

Db 85 LGDYDNRVVEPKNLDADKYKDYVDVFGANAYYQCAFSKKTINDINSHQTDKRTKCMYGG 144
Qy 111 VTLHDNRLTEKKVPIINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGQLDKYRSITVRVPEDGK-NLLSFD-VQYNKKKCVTAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKVQVGLIYVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKF--IENQNEFYDMMPPAGDKFDQSKYLMYNDNKMVDSKDVKLEV 258
Qy 229 YLYT 232
Db 259 YLTT 262

RESULT 82
US-10-428-817A-171
; Sequence 171, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 171
; LENGTH: 260
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-171

Query Match 21.6%; Score 267.5; DB 16; Length 260;
Best Local Similarity 33.1%; Pred. No. 4.4e-16;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

Qy 5 BEINEKDLRKSELQNALSNLROIYYNNEKAITENKESDDQFLENTLLFKGFFTGHFWY 64
Db 35 EQLN-----KSSQFTGVGNLRLCYDHNHVEGTNRSTQQLLQHDLIFFPKDLKLKNY 87
Qy 65 NDLLVLDLGSKDATNKYKGGKVDLYGAYVGYCAGGTEN-----KTACMYGGVTLHDNNRL 119
Db 88 DSVTEFNSKDLAAKYKNKQVDIFGSYNYNCYISEGNSCKNAKTCMYGGVTEHNRQI 147
Qy 120 TEKKVPIINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDFG 176
Db 148 --EGKFP-NITVKYVEDNENILSFD-ITTNKKQVTVQELDCKTRKILVSRKNLYEFNN-- 201
Qy 177 GKVQVGLIYVPHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLIDL 230
Db 202 SPYETGYIKFTESSGDSFWYDMMPPAGPAIFDQSKYLMYNDNKTIVSSSAIAIEVHL 257

RESULT 83
US-09-870-759-12
; Sequence 12, Application US/09870759
; Patent No. US20020177551A1

Db 27 AESQDPPTDELHAKSKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVGLSGKDATNKYKGGKVDLYGAYYGYQC-----AGTNPNTACTMYGGVTL 113
Db 85 LKNYDKVTTELLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGKVGKGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSNLHIDL 229
Db 203 FNS--SFYETGYIKFTIENNGTFTWYDMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 89
US-10-002-784A-14
; Sequence 14, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33
; APPLICANT: Ulrich, Robert G.
; TITLE OF INVENTION: Bacterial Superantigen Vaccines
; FILE REFERENCE: 003/233/SAP
; CURRENT APPLICATION NUMBER: US/10/002,784A
; PRIOR FILING DATE: 2001-11-26
; PRIOR APPLICATION NUMBER: 08/882,431; 09/144,776
; PRIOR FILING DATE: 97-06-25; 98-09-01
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 14
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: staphylococcal enterotoxin C-1 mutant
US-10-002-784A-14

Query Match 20.9%; Score 258.5; DB 14; Length 266;
Best Local Similarity 30.0%; Pred. No. 3e-15;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;
Qy 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKSDDOFLENTLLFKGFFTG 60
Db 27 AESQDPPTDELHAKSKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVGLSGKDATNKYKGGKVDLYGAYYGYQC-----AGTNPNTACTMYGGVTL 113
Db 85 LKNYDKVTTELLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGKVGKGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSNLHIDL 229
Db 203 FNS--SFYETGYIKFTIENNGTFTWYDMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 90
US-10-767-687-14
; Sequence 14, Application US/10767687
; Publication No. US20050064526A1
; GENERAL INFORMATION:

APPLICANT: Robert G. Ulrich,
Mark A. Olson
Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Charles H. Harris
STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent At
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA: US/10/767,687
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Charles H. Harris
REGISTRATION NUMBER: 34,616
REFERENCE/DOCKET NUMBER: <Unknown>
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 619-2065
TELEFAX: (301) 619-7714
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 266
TYPE: Amino Acid
STRANDEDNESS: Unknown
TOPOLOGY: Unknown
MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-767-687-14

Query Match 20.9%; Score 258.5; DB 17; Length 266;
Best Local Similarity 30.0%; Pred. No. 3e-15;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;
Qy 1 SEKSEINEKDLRKKSSELQARNLSNLROIYYNEKAITENKSDDOFLENTLLFKGFFTG 60
Db 27 AESQDPPTDELHAKSKF-TGLMENMKVLYDDHYVSATKVK-SVDKFRADHLIYNISDKK 84
Qy 61 HPWYNDLLVGLSGKDATNKYKGGKVDLYGAYYGYQC-----AGTNPNTACTMYGGVTL 113
Db 85 LKNYDKVTTELLNEGLAKKYKDEVDVYGSYVNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNNRLTEB--KKVPINLWDGQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKKNLYE 202
Qy 172 SDSFGKVGKGLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSNLHIDL 229
Db 203 FNS--SFYETGYIKFTIENNGTFTWYDMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVH 260
Qy 230 LYT 232
Db 261 LTT 263
RESULT 91
US-10-002-784A-26
; Sequence 26, Application US/10002784A
; Publication No. US20030036644A1
; GENERAL INFORMATION:
/33


```

; TITLE OF INVENTION: SUPERANTIGENS
; FILE REFERENCE: 12669-004001
; CURRENT APPLICATION NUMBER: US/10/997,690
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 09/869,136
; PRIOR FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: PCT/N299/00228
; PRIOR FILING DATE: 1999-12-24
; PRIOR APPLICATION NUMBER: NZ 333589
; PRIOR FILING DATE: 1998-12-24
; NUMBER OF SEQ ID NOS: 25
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 233
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-997-690-2

Query Match      20.7%; Score 256; DB 18; Length 233;
Best Local Similarity 27.4%; Pred. No. 4.3e-15;
Matches 66; Conservative 51; Mismatches 58; Indels 66; Gaps 10;

QY 17 ELQRLNALNLRIOIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD-----70
Db 26 EVDNNSL--LRNIY-----STIYVE-----YSDIVIDFKTSHN 56
QY 71 -----LGSKDATNKYKGVLDLYGAY-----YGYOCAGGTENKTACMYG 109
Db 57 LVTKKLDVRDARDFFINSEMDSYAANDFKTGKIAVSPFPDWNLYLSKG---KVTAYTYG 113
QY 110 GVTLLDNNRLTEBEKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGFL 169
Db 114 GITPYQKTSI--PKNIPVNLWINGKQISVYNEISTNKTITVTAQEDLKVRFELIAQHQL 171
QY 170 YNSDSFGKVGKQGLIVFHSSEGS--TVSYDLFQAQGYPDTLRIYRDNKTINSENL-HID 227
Db 172 YSS---GSSYKSGRLVFTNDNSDKYSFDLVGVYGRDKESIPKVKYDNKSFNIDKIGHLD 228
QY 228 L 228
Db 229 I 229

RESULT 95
US-09-870-759-20
; Sequence 20, Application US/09870759
; Patent No. US20020177551A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 870759
; CURRENT APPLICATION NUMBER: US/09/870,759
; CURRENT FILING DATE: 2002-01-14
; PRIOR APPLICATION NUMBER: US 60/208,128
; PRIOR FILING DATE: 2000-05-30
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-870-759-20

Query Match      19.8%; Score 245; DB 9; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KXSELQRLNALNLRIOIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 35 KPSQLQRLSNLVTFKIYIFFPMRVTLVTHENVKSVQDLSHDLIYN---VSGPNYDKLKTE 91
QY 71 LGSKDATNKYKGVLDLYGAYGYQC--AGGTPNKATACMYGGVTLHDNNRLTEBEKVPINL 129
Db 229 I 229

RESULT 96
US-09-870-759-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20

Query Match      19.8%; Score 245; DB 10; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KXSELQRLNALNLRIOIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 35 KPSQLQRLSNLVTFKIYIFFPMRVTLVTHENVKSVQDLSHDLIYN---VSGPNYDKLKTE 91
QY 71 LGSKDATNKYKGVLDLYGAYGYQC--AGGTPNKATACMYGGVTLHDNNRLTEBEKVPINL 129
Db 92 LKQEMATLFDKQKNDVIYGVYHLYCYLECENASACLYGGVTNHEGHNLEIPKIVVKV 151
QY 130 WIDGKQT--TVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGKQGLIVFHS 188
Db 152 SIDGIQSLSFDEIQKNG---NCSRISYTVRKYLTDNKLQYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSYDLFD-----AQGYPDTLRIYRDNKTINSENLHIDLXYLT 232
Db 206 KNKESFWDFPFPEPTOSKY----LMIYKDNETLDSNTSQIEVYLTT 249

RESULT 97
US-10-428-817A-16
; Sequence 16, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
```

```

Db 92 LKQEMATLFDKQKNDVIYGVYHLYCYLECENASACLYGGVTNHEGHNLEIPKIVVKV 151
QY 130 WIDGKQT--TVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGKQGLIVFHS 188
Db 152 SIDGIQSLSFDEIQKNG---NCSRISYTVRKYLTDNKLQYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSYDLFD-----AQGYPDTLRIYRDNKTINSENLHIDLXYLT 232
Db 206 KNKESFWDFPFPEPTOSKY----LMIYKDNETLDSNTSQIEVYLTT 249

RESULT 96
US-09-751-708A-20
; Sequence 20, Application US/09751708A
; Publication No. US20030157113A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 751708
; CURRENT APPLICATION NUMBER: US/09/751,708A
; CURRENT FILING DATE: 2002-10-15
; PRIOR APPLICATION NUMBER: US 60/173,371
; PRIOR FILING DATE: 1999-12-28
; NUMBER OF SEQ ID NOS: 166
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-751-708A-20

Query Match      19.8%; Score 245; DB 10; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KXSELQRLNALNLRIOIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 35 KPSQLQRLSNLVTFKIYIFFPMRVTLVTHENVKSVQDLSHDLIYN---VSGPNYDKLKTE 91
QY 71 LGSKDATNKYKGVLDLYGAYGYQC--AGGTPNKATACMYGGVTLHDNNRLTEBEKVPINL 129
Db 92 LKQEMATLFDKQKNDVIYGVYHLYCYLECENASACLYGGVTNHEGHNLEIPKIVVKV 151
QY 130 WIDGKQT--TVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKVGKQGLIVFHS 188
Db 152 SIDGIQSLSFDEIQKNG---NCSRISYTVRKYLTDNKLQYTNGP--SKYETGYIKFIP 205
QY 189 SEGSTVSYDLFD-----AQGYPDTLRIYRDNKTINSENLHIDLXYLT 232
Db 206 KNKESFWDFPFPEPTOSKY----LMIYKDNETLDSNTSQIEVYLTT 249

RESULT 97
US-10-428-817A-16
; Sequence 16, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
```

```
; PRIOR FILING DATE: 2002-10-02
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 16
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-16

Query Match      19.8%; Score 245; DB 16; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 35 KPSQLQRSLNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 91
Qy 71 LGSXDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGVTLLHDNNRLTEEEKVPINL 129
Db 92 LKQEMATLFDKKNVDIYGVYHLYCENAEASACLYGGVTNHEGHNLEIPKKIVVKV 151
Qy 130 WIDSKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGKVGQRLVPHS 188
Db 152 SIDGIQSLSFIDIEQKNG---NCSRSISYTVRKYLTDNKNQLYTNGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLFD---AQGYPDTLRLIYRDNKTNSLENHLDLYLT 232
Db 206 KKNESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 98
US-10-937-758A-20
; Sequence 20, Application US/10937758A
; Publication No. US20050112141A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: FILE REFERENCE 650884
; CURRENT APPLICATION NUMBER: US/10/937,758A
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: 09/650,884
; PRIOR FILING DATE: 2000-08-30
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 250
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-937-758A-20

Query Match      19.8%; Score 245; DB 17; Length 250;
Best Local Similarity 30.7%; Pred. No. 4.8e-14;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 35 KPSQLQRSLNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 91
Qy 71 LGSXDATNKYKGGKVDLYGAYGYQC-AGGTPNKACMYGVTLLHDNNRLTEEEKVPINL 129
Db 92 LKQEMATLFDKKNVDIYGVYHLYCENAEASACLYGGVTNHEGHNLEIPKKIVVKV 151
Qy 130 WIDSKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGYNSDSFGKVGQRLVPHS 188
Db 152 SIDGIQSLSFIDIEQKNG---NCSRSISYTVRKYLTDNKNQLYTNGP--SKYETGYIKFIP 205
Qy 189 SEGSTVSVDLFD---AQGYPDTLRLIYRDNKTNSLENHLDLYLT 232
Db 206 KKNESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 249

RESULT 99
US-10-428-817A-169
; Sequence 169, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
; PRIOR APPLICATION NUMBER: US 60/406,750
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: US 60/415,310
; PRIOR FILING DATE: 2002-10-01
; PRIOR APPLICATION NUMBER: US 60/415,400
; PRIOR APPLICATION NUMBER: US 60/438,686
; PRIOR FILING DATE: 2003-01-09
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 169
; LENGTH: 209
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-10-428-817A-169

Query Match      19.3%; Score 239; DB 16; Length 209;
Best Local Similarity 27.0%; Pred. No. 1.3e-13;
Matches 65; Conservative 48; Mismatches 62; Indels 56; Gaps 10;

Qy 17 ELQRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLLVD----- 70
Db 2 EVDNLSL-LRNIY-----STIVVE-----YSDTVIDPFKTSNN 32
Qy 71 -----LGSKDATNKYKGGKVDLYCAY-----YGVQACAGGTPNKACMYG 109
Db 33 LVTKKLDVRDARDPFINSEMDYAADFKAGDKIAVSPDPWNYLSKG---KVTAYTYG 89
Qy 110 GVTLLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFG 169
Db 90 GITPYQKTSI--PKNIPVNLWLNKQIPVPVQINQISTNKTVTTAQEIDLKVRKFLIAHQ 147
Qy 170 YNSDSFGKVGQRLVPHSSEGS-TVSVDLFDAGQYDPDTLRLIYRDNKTNSLENH-HID 227
Db 148 YSS---GSSYKSGKLVFHTNDNSDKYSLDLFYTGDRKESIFKVVYKDNKSFNIDKIGH 204
Qy 228 L 228
Db 205 I 205

RESULT 100
US-10-428-817A-184
; Sequence 184, Application US/10428817A
; Publication No. US20040214783A1
; GENERAL INFORMATION:
; APPLICANT: TERMAN, David S
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: 38373-189118
; CURRENT APPLICATION NUMBER: US/10/428,817A
; CURRENT FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: US 60/378,988
; PRIOR FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US 60/389,366
; PRIOR FILING DATE: 2002-06-15
; PRIOR APPLICATION NUMBER: US 60/406,697
; PRIOR FILING DATE: 2002-08-28
```


This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 11:01:24 ; Search time 22 Seconds
(without alignments)
790.601 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKDLKKSELR.....RDNKTINSENLHLYLTYT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

Issued Patents AA:*

1: /cgn2_6/prodata/1/aaa/5A-COMB.pep:*

2: /cgn2_6/prodata/1/aaa/5B-COMB.pep:*

3: /cgn2_6/prodata/1/aaa/6A-COMB.pep:*

4: /cgn2_6/prodata/1/aaa/6B-COMB.pep:*

5: /cgn2_6/prodata/1/aaa/PCUS-COMB.pep:*

6: /cgn2_6/prodata/1/aaa/backfilesi.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	233	4	US-08-695-692B-8
2	1238	100.0	257	3	US-08-486-099-112
3	1238	100.0	257	3	US-08-360-107A-122
4	1238	100.0	257	3	US-08-484-223B-112
5	1238	100.0	257	3	US-08-919-597-112
6	1238	100.0	257	3	US-08-475-668A-112
7	1238	100.0	257	3	US-08-485-551A-112
8	1238	100.0	257	3	US-08-471-913A-112
9	1238	100.0	257	3	US-08-485-264A-112
10	1238	100.0	257	3	US-08-474-349A-112
11	1238	100.0	257	4	US-08-470-896-112
12	1238	100.0	257	4	US-08-485-546A-112
13	1238	100.0	257	4	US-08-487-266A-112
14	1202	97.1	254	4	US-09-350-841A-1598
15	1171	94.6	226	3	US-08-896-933-24
16	1171	94.6	226	3	US-09-314-235-24
17	1171	94.6	226	4	US-09-708-008B-24
18	1023	82.6	233	4	US-08-695-692B-7
19	1023	82.6	257	3	US-08-486-099-113
20	1023	82.6	257	3	US-08-360-107A-123
21	1023	82.6	257	3	US-08-484-223B-113
22	1023	82.6	257	3	US-08-919-597-113
23	1023	82.6	257	3	US-08-475-668A-113
24	1023	82.6	257	3	US-08-485-551A-113
25	1023	82.6	257	3	US-08-471-913A-113
26	1023	82.6	257	3	US-08-485-264A-113
27	1023	82.6	257	3	US-08-474-349A-113

28	1023	82.6	257	4	US-08-470-896-113	Sequence 113, Appl
29	1023	82.6	257	4	US-08-485-546A-113	Sequence 113, Appl
30	1023	82.6	257	4	US-08-487-266A-113	Sequence 113, Appl
31	1019	82.3	233	1	US-08-446-918A-4	Sequence 4, Appl1
32	1019	82.3	233	2	US-08-580-806-4	Sequence 4, Appl1
33	1003.5	81.1	232	3	US-08-896-933-23	Sequence 23, Appl
34	1003.5	81.1	232	3	US-09-314-235-23	Sequence 23, Appl
35	1003.5	81.1	232	3	US-09-708-008B-23	Sequence 23, Appl
36	1000	80.8	257	3	US-09-144-776B-2	Sequence 2, Appl1
37	1000	80.8	257	3	US-08-882-431B-2	Sequence 2, Appl1
38	996	80.5	233	3	US-09-144-776B-4	Sequence 4, Appl1
39	996	80.5	233	3	US-08-882-431B-4	Sequence 4, Appl1
40	926.5	74.8	252	4	US-09-350-841A-1599	Sequence 1599, Ap
41	657	53.1	228	3	US-08-896-933-25	Sequence 25, Appl
42	657	53.1	228	3	US-09-314-235-25	Sequence 25, Appl
43	657	53.1	228	4	US-09-708-008B-25	Sequence 25, Appl
44	457	36.9	82	3	US-09-144-776B-19	Sequence 19, Appl
45	457	36.9	82	3	US-08-882-431B-19	Sequence 19, Appl
46	399	32.2	82	3	US-09-144-776B-17	Sequence 17, Appl
47	399	32.2	82	4	US-08-882-431B-17	Sequence 17, Appl
48	300	24.2	255	1	US-08-446-918A-2	Sequence 2, Appl1
49	300	24.2	255	2	US-08-580-806-2	Sequence 2, Appl1
50	296.5	23.9	221	3	US-08-896-933-29	Sequence 29, Appl
51	296.5	23.9	221	3	US-09-314-235-29	Sequence 29, Appl
52	296.5	23.9	221	4	US-09-708-008B-29	Sequence 29, Appl
53	294.5	23.8	251	4	US-08-973-391C-13	Sequence 13, Appl
54	293.5	23.7	266	3	US-09-144-776B-6	Sequence 6, Appl1
55	293.5	23.7	266	4	US-08-882-431B-6	Sequence 6, Appl1
56	292.5	23.6	239	3	US-08-896-933-26	Sequence 26, Appl
57	292.5	23.6	239	3	US-09-314-235-26	Sequence 26, Appl
58	292.5	23.6	239	4	US-09-708-008B-26	Sequence 26, Appl
59	292.5	23.6	266	3	US-09-414-276-8	Sequence 8, Appl1
60	291.5	23.5	221	4	US-08-973-391C-14	Sequence 14, Appl
61	289.5	23.4	251	3	US-09-144-776B-16	Sequence 16, Appl
62	289.5	23.4	251	4	US-08-882-431B-16	Sequence 16, Appl
63	288.5	23.3	239	3	US-09-144-776B-10	Sequence 10, Appl
64	288.5	23.3	239	4	US-08-882-431B-10	Sequence 10, Appl
65	282.5	22.8	266	3	US-09-144-776B-8	Sequence 8, Appl1
66	282.5	22.8	266	4	US-08-882-431B-8	Sequence 8, Appl1
67	281.5	22.7	238	3	US-08-896-933-28	Sequence 28, Appl
68	281.5	22.7	238	3	US-09-314-235-28	Sequence 28, Appl
69	281.5	22.7	238	4	US-09-708-008B-28	Sequence 28, Appl
70	267.5	21.6	239	3	US-08-896-933-27	Sequence 27, Appl
71	267.5	21.6	239	3	US-09-314-235-27	Sequence 27, Appl
72	267.5	21.6	239	4	US-09-708-008B-27	Sequence 27, Appl
73	260.5	21.0	239	3	US-08-896-933-21	Sequence 21, Appl
74	260.5	21.0	239	4	US-09-314-235-21	Sequence 21, Appl
75	260.5	21.0	239	4	US-09-708-008B-21	Sequence 21, Appl
76	258.5	20.9	266	3	US-09-144-776B-14	Sequence 14, Appl
77	258.5	20.9	266	4	US-08-882-431B-14	Sequence 14, Appl
78	245	19.8	220	3	US-08-896-933-20	Sequence 20, Appl
79	245	19.8	220	3	US-09-314-235-20	Sequence 20, Appl
80	245	19.8	220	4	US-09-708-008B-20	Sequence 20, Appl
81	215	17.4	82	3	US-09-144-776B-18	Sequence 18, Appl
82	215	17.4	82	4	US-08-882-431B-18	Sequence 18, Appl
83	191	15.4	45	1	US-08-220-378-1	Sequence 1, Appl1
84	191	15.4	45	2	US-08-696-012-1	Sequence 1, Appl1
85	183.5	14.8	235	4	US-09-336-036-2	Sequence 2, Appl1
86	183.5	14.8	235	4	US-09-308-829-2	Sequence 2, Appl1
87	181.5	14.7	208	3	US-08-896-933-30	Sequence 30, Appl
88	181.5	14.7	208	3	US-09-314-235-30	Sequence 30, Appl
89	181.5	14.7	208	4	US-09-708-008B-30	Sequence 30, Appl
90	137.5	11.1	89	3	US-09-144-776B-20	Sequence 20, Appl
91	137.5	11.1	89	4	US-08-882-431B-20	Sequence 20, Appl
92	129	10.4	28	1	US-08-220-378-2	Sequence 2, Appl1
93	129	10.4	28	2	US-08-696-012-2	Sequence 2, Appl1
94	127	10.3	24	3	US-08-838-413A-22	Sequence 22, Appl
95	126	10.2	23	1	US-08-220-378-5	Sequence 5, Appl1
96	126	10.2	23	2	US-08-696-012-5	Sequence 5, Appl1
97	124	10.0	29	1	US-08-220-378-6	Sequence 6, Appl1
98	124	10.0	29	2	US-08-696-012-6	Sequence 6, Appl1
99	121	9.8	79	3	US-09-144-776B-24	Sequence 24, Appl
100	121	9.8	79	4	US-08-882-431B-24	Sequence 24, Appl

101 120 9.7 22 1 US-08-220-378-4 Sequence 4, Appl
102 120 9.7 22 2 US-08-696-012-4 Sequence 4, Appl
103 112.5 9.1 89 3 US-09-144-776B-22 Sequence 22, Appl
104 112.5 9.1 89 3 US-09-144-776B-23 Sequence 23, Appl
105 112.5 9.1 89 4 US-08-882-431B-22 Sequence 22, Appl
106 112.5 9.1 89 4 US-08-882-431B-23 Sequence 23, Appl
107 111.5 9.0 443 3 US-09-710-279-1860 Sequence 1860, Ap
108 110.5 9.0 444 3 US-09-134-001C-4346 Sequence 4346, Ap
109 110 8.9 23 1 US-08-220-378-10 Sequence 10, Appl
110 110 8.9 23 2 US-08-696-012-10 Sequence 10, Appl
111 109 8.8 27 3 US-08-896-933-34 Sequence 34, Appl
112 109 8.8 27 3 US-09-314-235-34 Sequence 34, Appl
113 109 8.8 27 4 US-09-708-008B-34 Sequence 34, Appl
114 109 8.8 193 3 US-08-896-933-31 Sequence 31, Appl
115 109 8.8 193 3 US-09-314-235-31 Sequence 31, Appl
116 109 8.8 193 4 US-09-708-008B-31 Sequence 31, Appl
117 109 8.8 229 4 US-09-350-841A-1597 Sequence 1597, Ap
118 107.5 8.7 234 3 US-08-486-099-111 Sequence 111, App
119 107.5 8.7 234 3 US-08-360-107A-121 Sequence 121, App
120 107.5 8.7 234 3 US-08-484-223B-111 Sequence 111, App
121 107.5 8.7 234 3 US-08-919-537-111 Sequence 111, App
122 107.5 8.7 234 3 US-08-475-668A-111 Sequence 111, App
123 107.5 8.7 234 3 US-08-485-551A-111 Sequence 111, App
124 107.5 8.7 234 3 US-08-471-913A-111 Sequence 111, App
125 107.5 8.7 234 3 US-08-485-264A-111 Sequence 111, App
126 107.5 8.7 234 3 US-08-474-349A-111 Sequence 111, App
127 107.5 8.7 234 4 US-08-470-896-111 Sequence 111, App
128 107.5 8.7 234 4 US-08-485-546A-111 Sequence 111, App
129 107.5 8.7 234 4 US-08-487-266A-111 Sequence 111, App
130 106.5 8.6 29 1 US-08-220-378-9 Sequence 9, Appl
131 106.5 8.6 29 2 US-08-696-012-9 Sequence 9, Appl
132 106 8.6 28 1 US-08-220-378-7 Sequence 7, Appl
133 106 8.6 28 2 US-08-696-012-7 Sequence 7, Appl
134 105.5 8.5 89 3 US-09-144-776B-21 Sequence 21, Appl
135 105.5 8.5 89 4 US-08-882-431B-21 Sequence 21, Appl
136 105.5 8.5 194 1 US-08-446-918A-6 Sequence 6, Appl
137 105.5 8.5 194 2 US-08-580-806-6 Sequence 3, Appl
138 105 8.5 25 1 US-08-220-378-3 Sequence 3, Appl
139 105 8.5 25 2 US-08-696-012-3 Sequence 12, Appl
140 104.5 8.4 234 3 US-09-144-776B-12 Sequence 12, Appl
141 104.5 8.4 234 4 US-08-882-431B-12 Sequence 12, Appl
142 100.5 8.1 234 1 US-08-152-456A-2 Sequence 2, Appl
143 100.5 8.1 234 1 US-08-440-221-2 Sequence 8, Appl
144 100 8.1 28 1 US-08-220-378-8 Sequence 8, Appl
145 100 8.1 28 2 US-08-696-012-8 Sequence 4674, Ap
146 94.5 7.6 402 3 US-09-134-001C-4674 Sequence 111, App
147 93.5 7.6 631 1 US-08-487-890A-111 Sequence 111, App
148 93.5 7.6 631 2 US-08-478-435-111 Sequence 111, App
149 93.5 7.6 631 2 US-08-337-483-111 Sequence 111, App
150 93.5 7.6 631 3 US-08-478-373-111 Sequence 111, App
151 93.5 7.6 631 3 US-08-474-671-111 Sequence 111, App
152 93.5 7.6 631 3 US-08-483-577A-111 Sequence 111, App
153 93.5 7.6 631 3 US-08-897-438-111 Sequence 111, App
154 93.5 7.6 631 3 US-08-637-654-111 Sequence 111, App
155 93.5 7.6 631 3 US-08-649-518-111 Sequence 111, App
156 93 7.5 16 4 US-08-695-692B-20 Sequence 20, Appl
157 93 7.5 28 3 US-08-896-933-22 Sequence 22, Appl
158 93 7.5 28 3 US-09-314-235-22 Sequence 22, Appl
159 93 7.5 28 4 US-09-708-008B-22 Sequence 22, Appl
160 92.5 7.5 337 4 US-09-248-796A-16723 Sequence 16723, A
161 92.5 7.5 1183 4 US-09-532-310B-5 Sequence 5, Appl
162 89.5 7.2 36 3 US-08-838-413A-7 Sequence 7, Appl
163 89.5 7.2 38 3 US-08-838-413A-8 Sequence 8, Appl
164 89 7.2 24 3 US-08-838-413A-18 Sequence 18, Appl
165 89 7.2 171 4 US-09-710-279-1074 Sequence 1074, Ap
166 89 7.2 179 3 US-09-134-001C-3300 Sequence 3300, Ap
167 89 7.2 317 4 US-09-248-796A-19212 Sequence 19212, A
168 89 7.2 631 1 US-08-487-890A-115 Sequence 115, App
169 89 7.2 631 2 US-08-478-435-115 Sequence 115, App
170 89 7.2 631 2 US-08-337-483-115 Sequence 115, App
171 89 7.2 631 2 US-08-478-373-115 Sequence 115, App
172 89 7.2 631 3 US-08-474-671-115 Sequence 115, App
173 89 7.2 631 3 US-08-483-577A-115 Sequence 115, App

Sequence 115, App
Sequence 115, App
Sequence 115, App
Sequence 19860, A
Sequence 4103, Ap
Sequence 4002, Ap
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 1166, Ap
Sequence 3752, Ap
Sequence 11, Appl
Sequence 16, Appl
Sequence 14871, A
Sequence 4547, Ap
Sequence 2, Appl
Sequence 6514, Ap
Sequence 1138, Ap
Sequence 4023, Ap

7.2 631 3 US-08-897-438-115
7.2 631 3 US-08-637-654-115
7.2 631 3 US-08-649-518-115
7.1 629 4 US-09-248-796A-19860
7.0 286 3 US-09-134-001C-4103
7.0 834 1 US-09-107-532A-4002
7.0 834 2 US-08-471-033-21
7.0 834 2 US-08-471-044-21
7.0 834 2 US-08-463-483A-21
7.0 834 2 US-08-471-046A-21
7.0 834 2 US-08-470-566B-21
7.0 834 2 US-08-469-334-21
7.0 834 3 US-09-300-529-21
6.9 17 3 US-08-896-933-10
6.9 17 3 US-09-314-235-10
6.9 17 4 US-09-708-008B-10
6.8 228 4 US-09-710-279-1166
6.8 406 4 US-09-134-000C-3752
6.8 1588 5 PCT-US93-07261-11
6.8 1663 5 PCT-US93-07261-16
6.8 365 3 US-09-134-001C-4412
6.8 558 4 US-09-902-540-14971
6.8 675 3 US-09-134-001C-4547
6.8 1014 4 US-09-762-724-2
6.7 251 4 US-09-543-681A-6514
6.7 752 4 US-09-710-279-1138
6.7 767 3 US-09-134-001C-4023

ALIGNMENTS

RESULT 1
US-08-695-692B-8
; Sequence 8, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlaten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHEMIC SUPERANTIGENS
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695,692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-695-692B-8

Query Match 100.0%; Score 1238; DB 4; Length 233;
Best Local Similarity 100.0%; Pred. No. 9.3e-119; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;
QY 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233
DB 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233

RESULT 2

US-08-486-099-112
Sequence 112, Application US/08486099
Patent No. 6013263
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
TITLE OF INVENTION: B VIRUS TRANSMISSION
NUMBER OF SEQUENCES: 209
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,099
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-031
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 112:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-486-099-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233
DB 205 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 3

US-08-360-107A-122
Sequence 122, Application US/08360107A
Patent No. 6017536
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 149
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/360,107A
FILING DATE: 20-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-013
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 122:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-360-107A-122

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;

Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 25 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
Qy 61 HPWYNDLLVLDGSDATNKYKGVLDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSDATNKYKGVLDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 4
US-08-484-223B-112
; Sequence 112, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

Db 25 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
Qy 61 HPWYNDLLVLDGSDATNKYKGVLDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSDATNKYKGVLDLYGAYYGQAGGTPNKACMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 5
US-08-919-597-112
; Sequence 112, Application US/08919597
; Patent No. 6054265
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/919,597
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/470,896
; FILING DATE: 06-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-919-597-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60

Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 6

US-08-475-668A-112
; Sequence 112, Application US/08475668A
; Patent No. 6060065
; GENERAL INFORMATION:
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,668A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-026
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-475-668A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
Db 205 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 257

RESULT 7

US-08-485-551A-112
; Sequence 112, Application US/08485551A
; Patent No. 6068973
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,551A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-023
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-551A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQCAGTGNKTAACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 233
|
Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 8
US-08-471-913A-112
; Sequence 112, Application US/08471913A
; Patent No. 6093794
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
; TITLE OF INVENTION: TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US/08/471.913A
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-030
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-471-913A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFPTG 60
|
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFPTG 84
|
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYYQCAGGTENKTACMYGGVTLHDNNRLT 120
|
Db 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYYQCAGGTENKTACMYGGVTLHDNNRLT 144
|
Qy 121 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
|
Db 145 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
|
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 233
|

Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 9
US-08-485-264A-112
; Sequence 112, Application US/08485264A
; Patent No. 6228983
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Dennis M.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING
; TITLE OF INVENTION: RESPIRATORY SYNCYTIAL VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 232
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485.264A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-021
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-485-264A-112

Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFPTG 60
|
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNKAITENKESDDQFLENTLLPKGFPTG 84
|
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYYQCAGGTENKTACMYGGVTLHDNNRLT 120
|
Db 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYYQCAGGTENKTACMYGGVTLHDNNRLT 144
|
Qy 121 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
|
Db 145 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
|
Qy 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 233
|
Db 205 RGLIVFHSSEGSTVSYDLFDAQGOYPTDLLRIYRDNKTINSENHLIDLYLTT 257

RESULT 10
US-08-474-349A-112
; Sequence 112, Application US/08474349A
; Patent No. 6333395
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HUMAN PARAINFLUENZA
; TITLE OF INVENTION: VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 517
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/474,349A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-024
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-474-349A-112
Query Match 100.0%; Score 1238; DB 3; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELRQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELRQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHIDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHIDLYLYTT 257
RESULT 11
US-08-470-896-112
; Sequence 112, Application US/08470896

Patent No. 6479055
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Pettaway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 273
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/470,896
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-020
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-470-896-112
Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.1e-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSELRQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELRQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
DB 85 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144
QY 121 EEKKVPINLWDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 180
DB 145 EEKKVPINLWDGKQTTPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVKQ 204
QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHIDLYLYTT 233
DB 205 RGLIVFHSSEGSTSVSYDLFDAQQYQPDTLRIYRDNKTINSENHIDLYLYTT 257
RESULT 12
US-08-485-546A-112
; Sequence 112, Application US/08485546A
; Patent No. 6518013
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.

```
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 214
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/485,546A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-028
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-485-546A-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.le-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLTYTT 257

RESULT 13
US-08-487-266A-112
; Sequence 112, Application US/08487266A
; Patent No. 6824783
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.

; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; NUMBER OF SEQUENCES: 239
; CORRESPONDENCE ADDRESS:
; ADDRESS: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 112:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-487-266A-112

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.le-118;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFT 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLTYTT 257

RESULT 14
US-09-350-841A-1598
; Sequence 1598, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jeffes, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; CURRENT FILING DATE: 1999-07-09
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: PatentIn Ver. 2.1
```


; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 97.1%; Score 1202; DB 4; Length 254;
Best Local Similarity 98.3%; Pred. No. 5.2e-115;
Matches 230; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 22 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 81
QY 61 HPWYNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLT 120
DB 82 HPWYNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLT 141
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 180
DB 142 BEKVPINLWID-KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 200
QY 181 RGLIVFHSSEG-STVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 201 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 254

RESULT 15
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24

Query Match 94.6%; Score 1171; DB 3; Length 226;
Best Local Similarity 95.7%; Pred. No. 6.6e-112;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 4 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLTEK 123
DB 61 YNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLTEK 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 183
DB 120 ---VBKWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 176
QY 184 IVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 177 IVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 226

RESULT 17
US-09-708-008B-24
; Sequence 24, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; EARLIER FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-24

Query Match 94.6%; Score 1171; DB 4; Length 226;
Best Local Similarity 95.7%; Pred. No. 6.6e-112;

; SEQ ID NO 1598
; LENGTH: 254
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1598

Query Match 97.1%; Score 1202; DB 4; Length 254;
Best Local Similarity 98.3%; Pred. No. 5.2e-115;
Matches 230; Conservative 0; Mismatches 2; Indels 2; Gaps 2;

QY 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
DB 22 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 81
QY 61 HPWYNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLT 120
DB 82 HPWYNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLT 141
QY 121 BEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 180
DB 142 BEKVPINLWID-KQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 200
QY 181 RGLIVFHSSEG-STVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 201 RGLIVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 254

RESULT 15
US-08-896-933-24
; Sequence 24, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 24
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-24

Query Match 94.6%; Score 1171; DB 3; Length 226;
Best Local Similarity 95.7%; Pred. No. 6.6e-112;
Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;

QY 4 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 63
DB 1 SESEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPW 60
QY 64 YNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLTEK 123
DB 61 YNDLLVGLSKDATNKYKGGVDLYGAYGYOCAGTGNKTCMYGGVTLHNNRLTEK 119
QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 183
DB 120 ---VBKWDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVG 176
QY 184 IVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 233
DB 177 IVFHSSEGSTVSYDLFDAQQGYPTDLLRIYRDNKTINSENHLIDLYTT 226

RESULT 16
US-09-314-235-24
; Sequence 24, Application US/09314235
; Patent No. 6338845

Matches 220; Conservative 4; Mismatches 2; Indels 4; Gaps 1;
Qy 4 SEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHPW 63
Db 1 SEENEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHPW 60
Qy 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTBEK 123
Db 61 YNDLLVDKGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTBE- 119
Qy 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQGL 183
Db 120 ---VBKWIIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQGL 176
Qy 184 IVFHSSEGSTVSVDLFDAGQGOVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 177 IVFHSSEGSTVSVDLFDAGQGOVPTLLRIYRDNKTINSENHIDILYLYTT 226

RESULT 18
US-08-695-692B-7
; Sequence 7, Application US/08695692B
; Patent No. 6514498
; GENERAL INFORMATION:
; APPLICANT: Per Antonsson, Per Bjork, Mikael Dohlaten,
; APPLICANT: Johan Hansson, Terje Kalland, Lars
; APPLICANT: Abrahamson and Goran Forsberg
; TITLE OF INVENTION: MODIFIED/CHIMERIC SUPERANTIGENS
; TITLE OF INVENTION: AND THEIR USE
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pravel, Hewitt, Kimball & Krieger
; STREET: 1177 West Loop South, 10th Floor
; CITY: Houston
; STATE: TX
; COUNTRY: USA
; ZIP: 77027-9095
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/695.692B
; FILING DATE: August 12, 1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 9601245-5
; FILING DATE: March 29, 1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Krieger, Paul E.
; REGISTRATION NUMBER: 25,886
; REFERENCE/DOCKET NUMBER: 41986/1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 713-850-0909
; TELEFAX: 713-850-0165
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-695-692B-7

Query Match 82.6%; Score 1023; DB 4; Length 233;
Best Local Similarity 82.0%; Pred. No. 1e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHG 60
Db 1 SEKEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHG 60
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120

Db 61 HSWYNDLLVDPSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGKVGQ 180
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGOVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 181 RGLIVFHSSTEPSVNYDLFQAQGOYSNTLLRIYRDNKTINSENHIDILYLYTS 233
RESULT 19
US-08-486-099-113
; Sequence 113, Application US/08486099
; Patent No. 6013263
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HEPATITIS
; TITLE OF INVENTION: B VIRUS TRANSMISSION
; NUMBER OF SEQUENCES: 209
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486.099
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-031
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-486-099-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHG 60
Db 25 SEKEEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGPFTHG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDPSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

QY 121 EEKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLNLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHIDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDLYLTS 257

RESULT 20
US-08-360-107A-123
; Sequence 123, Application US/08360107A
; Patent No. 6017536
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION
; TITLE OF INVENTION: OF MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 149
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/360,107A
; FILING DATE: 20-DEC-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-013
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 123:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-360-107A-123

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLNLYNSDVDFGKQV 204

QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHIDLYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAGQYSNTLLRIYRDNKTINSENHIDLYLTS 257

RESULT 21
US-08-484-223B-113
; Sequence 113, Application US/08484223B
; Patent No. 6020459
; GENERAL INFORMATION:
; APPLICANT: Bolognesi, Dani P.
; APPLICANT: Matthews, Thomas J.
; APPLICANT: Wild, Carl T.
; APPLICANT: Barney, Shawn O.
; APPLICANT: Lambert, Dennis M.
; APPLICANT: Petteway, Stephen R.
; APPLICANT: Langlois, Alphonse J.
; TITLE OF INVENTION: COMPOSITIONS FOR INHIBITION OF
; TITLE OF INVENTION: MEMBRANE FUSION-ASSOCIATED EVENTS, INCLUDING HIV
; NUMBER OF SEQUENCES: 245
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds LLP
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,223B
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-029
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-484-223B-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOARNLSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 84
QY 61 HPWYNLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNLLVDFDSKDIDVKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EEKVPINLWDGKQNTVPLETVKTKNKNVTQELDLQARRYLQEKYLNLYNSDVDFGKQV 204
QY 181 RGLIVFHSSEGSTVSVDLFDAGQYPTDILLRIYRDNKTINSENHIDLYLTT 233

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDYGYGYQACGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIDVYKYGKVDLYGAYGYQACGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGKQV 180
DB 145 EKKVPINLWIDGKQTPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGKQV 204
QY 181 RGLIVPHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVPHSTEPSVNYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLT 257

RESULT 26
US-08-485-264A-113
Sequence 113, Application US/08485264A
Patent No. 6228983
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.

GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Pettaway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING INFLUENZA VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 211
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,551A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-023
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-551A-113

Query Match 82.6%; Score 1023; DB 3; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVLDGSKDATNKYKGVLDYGYGYQACGTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFPSKDIDVYKYGKVDLYGAYGYQACGTPNKTCMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGKQV 180
DB 145 EKKVPINLWIDGKQTPIDKVTSSKEVTVQELDLQARHYLHGKFGYNSDSFGKQV 204
QY 181 RGLIVPHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLT 233
DB 205 RGLIVPHSTEPSVNYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLT 257

RESULT 25
US-08-471-913A-113
Sequence 113, Application US/08471913A
Patent No. 6093794
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.

CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,896
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-020
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-470-896-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDLGSKDIDVYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNLYNSDVFPGKQV 204

QY 181 RGLVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLDLYLT 233
Db 205 RGLVPHSTSTEPSVNYDLFQAQGYNTLLRIYRDNKNTINSENHLDLYLT 257

RESULT 29
US-08-485-546A-113
Sequence 113, Application US/08485546A
Patent No. 6518013
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING EPSTEIN-BARR VIRUS
TITLE OF INVENTION: TRANSMISSION
NUMBER OF SEQUENCES: 214
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,546A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7872-028
TELEPHONE: (212) 869-9741/8864
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 113:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-485-546A-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDLGSKDIDVYKGGKVDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

QY 121 EKKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQV 180
Db 145 EKKVPINLWLDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNLYNSDVFPGKQV 204

QY 181 RGLVPHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKNTINSENHLDLYLT 233
Db 205 RGLVPHSTSTEPSVNYDLFQAQGYNTLLRIYRDNKNTINSENHLDLYLT 257

RESULT 30
US-08-487-266A-113
Sequence 113, Application US/08487266A
Patent No. 6824783
GENERAL INFORMATION:
APPLICANT: Bolognesi, Dani P.
APPLICANT: Matthews, Thomas J.
APPLICANT: Wild, Carl T.
APPLICANT: Barney, Shawn O.
APPLICANT: Lambert, Dennis M.
APPLICANT: Petteway, Stephen R.
APPLICANT: Langlois, Alphonse J.
TITLE OF INVENTION: METHODS FOR INHIBITION OF MEMBRANE
FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
TITLE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
NUMBER OF SEQUENCES: 239
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,266A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Coruzzi, Laura A.
; REGISTRATION NUMBER: 30,742
; REFERENCE/DOCKET NUMBER: 7872-025
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 869-9741/8864
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 113:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-487-266A-113

Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 1.2e-96;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 25 SEKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLNTLLFKGFFTD 84

Qy 61 HPWNLLVLDLGSKDATNKYKGVVLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKIDVDKYKGVVLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWDGKOTTPIDKVTSKKEVTVOELDLQARHVLHGKFLGYNDSFGGKVQ 180
Db 145 EEKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYNLNSVDVFDGKVQ 204

Qy 181 RGLIVFHSSEGSTSVSYDLFDAQGYQVPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 205 RGLIVFHTSTSPSYNDLFGAGQYSNTLLRIYRDNKTINSNMHIDIYLYTS 257

RESULT 31
US-08-446-918A-4
; Sequence 4, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,918A
; FILING DATE: 18-MAY-1995
; CLASSIFICATION: 552
; ATTORNEY/AGENT INFORMATION:

; NAME: Kovarik, Joseph E.
; REGISTRATION NUMBER: 33,005
; REFERENCE/DOCKET NUMBER: 2879-29
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-446-918A-4

Query Match 82.3%; Score 1019; DB 1; Length 233;
Best Local Similarity 81.9%; Pred. No. 2.6e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

Qy 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLNTLLFKGFFTG 61
Db 2 EKSEINEKDLRKSELQNALSNLRQIYYNNEKAITENKESDDQFLNTLLFKGFFTDH 61

Qy 62 PWYNDLLVLDLGSKDATNKYKGVVLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVDFDSKIDVDKYKGVVLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTE 121

Qy 122 EKKVPINLWDGKOTTPIDKVTSKKEVTVOELDLQARHVLHGKFLGYNDSFGGKVQ 181
Db 122 EKKVPINLWDGKQNTVPLETVTKNKNVTVQELDLQARRYLQEKYNLNSVDVFDGKVQ 181

Qy 182 GLIVFHSSEGSTSVSYDLFDAQGYQVPTDLLRIYRDNKTINSNLHIDLTYTT 233
Db 182 GLIVFHTSTSPSYNDLFGAGQYSNTLLRIYRDNKTINSNMHIDIYLYTS 233

RESULT 32
US-08-580-806-4
; Sequence 4, Application US/08580806
; Patent No. 5935568
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmslie, Robyn E.
; APPLICANT: Potter, Terence A.
; TITLE OF INVENTION: GENE THERAPY FOR EFFECTOR CELL REGULATION
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/580,806
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Connell, Gary J.
; REGISTRATION NUMBER: 32,020
; REFERENCE/DOCKET NUMBER: 2879-29-C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 863-9700
; TELEFAX: (303) 863-0223
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233 amino acids
; TYPE: amino acid
; TOPOLOGY: linear


```
; MOLECULE TYPE: protein
US-08-580-806-4

Query Match      82.3%; Score 1019; DB 2; Length 233;
Best Local Similarity 81.9%; Pred. No. 2.6e-96;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTDH 61

QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVDLGSKDIDVTKYKGGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLQEKYKLYNSDVDFGKQVOR 181

QY 182 GLIVFHSSEGSTVSYDLFDAQGYQPDTLRIYRDNKTINSENHLIDLYTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHIDVLYTS 233

RESULT 33
US-08-896-933-23
; Sequence 23, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-23

Query Match      81.1%; Score 1003.5; DB 3; Length 232;
Best Local Similarity 81.5%; Pred. No. 1e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTD 59

QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLT 120
DB 60 HSWYNDLLVDLGSKDIDVTKYKGGKVDLYGAYGYQCAGTGNKTAQMYGGVTLHDNNRLT 119

QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKQV 180
DB 120 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARHYLQEKYKLYNSDVDFGKQV 179

QY 181 RGLIVFHSSEGSTVSYDLFDAQGYQPDTLRIYRDNKTINSENHLIDLYTT 233
DB 180 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHIDVLYTS 232

RESULT 35
US-09-708-008B-23
; Sequence 23, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 23
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-23

Query Match      81.1%; Score 1003.5; DB 4; Length 232;
Best Local Similarity 81.5%; Pred. No. 1e-94;
Matches 190; Conservative 16; Mismatches 26; Indels 1; Gaps 1;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
```

Db 1 SEKSEINEKDLRKSELQGTALGNLQIYYNNEKAKTENKESHQFL-HTILPKGFPTD 59
Qy 61 HPWYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 60 HSWYNDLLVDFDSKDIYDKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 119
Qy 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 120 BEKKVPINLWDGKQNTVPLETVTKNKVTVQELDPOARRYLOEKYNLYNSDVFDGKVQ 179
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLHDLYLVT 233
Db 180 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHWHIDIYLYTS 232

RESULT 36
US-09-144-776B-2
; Sequence 2, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-144-776B-2

Query Match 80.8%; Score 1000; DB 3; Length 257;
Best Local Similarity 80.7%; Pred. No. 2.7e-94;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQGTALGNLQIYYNNEKAKTENKESHQFLHTILPKGFPTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLQIYYNNEKAKTENKESHQFLHTILPKGFPTD 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
Qy 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWDGKQNTVPLETVTKNKVTVQELDPOARRYLOEKYNLYNSDVFDGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLHDLYLVT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYQNTLLRIYRDNKTINSENHWHIDIYLYTS 257

RESULT 37
US-08-882-431B-2
; Sequence 2, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; Vaccines
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 257
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-2

Query Match 80.8%; Score 1000; DB 4; Length 257;
Best Local Similarity 80.7%; Pred. No. 2.7e-94;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELQGTALGNLQIYYNNEKAKTENKESHQFLHTILPKGFPTG 60
Db 25 SEKSEINEKDLRKSELQGTALGNLQIYYNNEKAKTENKESHQFLHTILPKGFPTD 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDIYDKYKGVKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 144
Qy 121 BEKKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Db 145 BEKKVPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVDFGKVQ 204
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
Db 205 RGLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHIDLYLTS 257

RESULT 38
US-09-144-776B-4
; Sequence 4, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-144-776B-4

Query Match 80.5%; Score 996; DB 3; Length 233;
Best Local Similarity 80.6%; Pred. No. 6e-94;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61
Db 2 EKSEINEKDLRKKSSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61
QY 62 PWNDDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDDLVRFDSDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKVKPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVDFGKVQ 181
Db 122 EKVKPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVDFGKVQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
Db 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTS 233

RESULT 40
US-09-350-841A-1599

Db 182 GLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHIDLYLTS 233

RESULT 39
US-08-882-431B-4
; Sequence 4, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 233
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-4

Query Match 80.5%; Score 996; DB 4; Length 233;
Best Local Similarity 80.6%; Pred. No. 6e-94;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKKSSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61
Db 2 EKSEINEKDLRKKSSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLFKGFPTGH 61
QY 62 PWNDDLVLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 62 SWYNDDLVRFDSDIYDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKVKPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVDFGKVQ 181
Db 122 EKVKPINLWLDGKQNTVPLETVTKNKNVTVQELDLQARRYLQKYNLYNSDVDFGKVQ 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLTT 233
Db 182 GLIVFHTSTEPSVNDLFGAQQYSNTLLRIYRDNKTINSENHIDLYLTS 233

```
; Sequence 1599, Application US/09350841A
; Patent No. 6750008
; GENERAL INFORMATION:
; APPLICANT: Jefe, Peter;
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITION OF MEMBRANE
; FILE OF INVENTION: FUSION-ASSOCIATED EVENTS, INCLUDING HIV TRANSMISSION
; FILE REFERENCE: 7872-066-999
; CURRENT APPLICATION NUMBER: US/09/350,841A
; NUMBER OF SEQ ID NOS: 1946
; SOFTWARE: Patentin ver. 2.1
; SEQ ID NO 1599
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-09-350-841A-1599

Query Match      74.8%; Score 926.5; DB 4; Length 252;
Best Local Similarity 79.1%; Pred. No. 8.9e-87;
Matches 185; Conservative 16; Mismatches 26; Indels 7; Gaps 6;

Qy 1 SEKSEETNEKDLRKSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLKGPFTG 60
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 25 SEKSEETNEKDLRKSELQGTALGNLQIYYNEKAKTENKESHDFLOHTILFKGPF 84
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 61 HPWYNDLLVGLSGSDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 85 HSWYNDLLVDFDSK-IVDKY--KKCD-YGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 140
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 121 BEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVQ 180
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 141 BEKVPINLWIDGKQTTVPLETVKTNKKNVTVOELD-QARRYLOEK-NLYNSDVF 198
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 181 RGLVPHSSEGSTVSYDLFDA-QGQYPTLRIYRDNKTINSENHLIDLYLTT 233
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 199 RGLVPHSTPEFSYNDLFGAGQYQSYNTLRIYRDNKTINSENHIDLYLTS 252
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 41
US-08-896-933-25
Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-25

Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

Qy 7 INEKDLRKSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLKGPFTGHPWYND 66
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKFFTDLINP 61
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 67 LLDVGLSGSDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVP 126
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 LLINFNSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 127 INLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVORGLIVF 186
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 187 HSEGSTVSYDLFDAQGYQYPTLRIYRDNKTINSENHLIDLYL 231
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 182 DSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTEHLHIDLYL 226
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

US-08-896-933-25

Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

Qy 7 INEKDLRKSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLKGPFTGHPWYND 66
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKFFTDLINP 61
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 67 LLDVGLSGSDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVP 126
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 LLINFNSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 127 INLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVORGLIVF 186
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

US-08-896-933-25
```

```
Db 122 INLWINGVQKEVSLDKVQTDKKNVTVOELDAQARYLQKDLKLYNDTLGGKIQRGKIEF 181
Qy 187 HSEGSTVSYDLFDAQGYQYPTLRIYRDNKTINSENHLIDLYL 231
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 182 DSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTEHLHIDLYL 226
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 42
US-09-314-235-25
; Sequence 25, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 25
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-25

Query Match      53.1%; Score 657; DB 3; Length 228;
Best Local Similarity 55.6%; Pred. No. 3.2e-59;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0;

Qy 7 INEKDLRKSELQNALSNLRIQIYYNEKAITENKESDDQFLENTLLKGPFTGHPWYND 66
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 2 VKEKELHKKSELSTALNNMKHSYADKNPIIGENKSTGDOFLENTLLYKFFTDLINP 61
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 67 LLDVGLSGSDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLTEKKVP 126
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 LLINFNSKEMAQHFKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKLERKKIP 121
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 127 INLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGGKVORGLIVF 186
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 187 HSEGSTVSYDLFDAQGYQYPTLRIYRDNKTINSENHLIDLYL 231
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 182 DSDGSKVSYDLFDVKGDFPEKQLRIYSDNKTLSLSTEHLHIDLYL 226
Db |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

RESULT 43
US-09-708-008B-25
; Sequence 25, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-19

Query Match ..... 36.9%; Score 457; DB 4; Length 82;
Best Local Similarity 100.0%; Pred. No. 2.3e-39;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Qy      43 SDDQFLNTLLFKGFETHPWINDLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTN 102
         |||||
Db      1 SDDQFLNTLLFKGFETHPWINDLLVDLGSKDATNKYGGKVDLYGAYGYQCAGGTN 60

```

Qy 103 KTACMYGGVTLHDNNRLTEKK 124
Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 46

```

US-09-144-776B-17
; Sequence 17, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
;           Mark A. Olson
;           Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
;
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC - 504 Scott Street
;           MCMR-JA (Charles H. Harris-Patent
;           Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012

```

Query Match	32.2%	Score 399;	DB 3;	Length 82;
Best Local Similarity	86.6%;	Pred. No. 2.1e-33;		
Matches	71;	Conservative	4;	Mismatches 7; Indels 0; Gaps 0;

Qy	43	SDOQFLENTLLFKGFFTHGPWYNLDLVLGSKDANKYKGGKVLDLYGAYGYQCAAGTTPN	102
		: : : :	
Db	1	SHQDFLOHTILFKGFFTDHRSWYNLDLVDFOSKDIVDKYKGGKVLDLYGAYGYQCAAGTTPN	60

Qy	103	KTACMYGGVTLHDNNRLTEKK	124
Db	61	KTACMYGGVTLHDNNRLTEKK	82

RESULT 47

US-08-882-431B-17
; Sequence 17, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,

```

APPLICANT: Mark A. Olson
APPLICANT: Sina Bavari
TITLE OF INVENTION: Bacterial Superantigen
NUMBER OF INVENTIONS: Vaccines
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESS: Charles H. Harris
STREET: US Army MAMC -504 Scott Street MC
CITY: FORT DETRICK
STATE: MARYLAND
COUNTRY: USA
ZIP: 21702-5012
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 7.5
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/882,431B
FILING DATE: June 25, 1997
CLASSIFICATION:
PRIOR APPLICATION NUMBER:

```

Query Match 32.2%; Score 399; DB 4; Length 82;
Best Local Similarity 86.6%; Pred. No. 2.1e-33;
Matches 71; Conservative 4; Mismatches 7; Indels

Qy	43	SDQFLENTLLFKGFFFGHBYNDLLV	DLGSKD	ATNKYK	KKKVD	LYGAYGYQCAGGTPN	102
		:::					
Db	1	SHQDFLQHTLLFKGFFFDH	SWYNOLLV	DFDSK	DIVDKY	KKKVD	LYGAYGYQCAGGTPN 60
		:::					
Qy	103	KTACMGVGT	LHDNNRLTEKK	124			
Db	61	KTACMGVGT	LHDNNRLTEKK	82			

RESULT 48

```

US-08-446-918A-2
; Sequence 2, Application US/08446918A
; Patent No. 5705151
; GENERAL INFORMATION:
; APPLICANT: Dow, Steve W.
; APPLICANT: Elmallee, Robyn E.
; TITLE OF INVENTION: GENE THERAPY FOR T CELL REGULATION
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Sheridan Ross & McIntosh
; STREET: 1700 Lincoln Street, Suite 3500
; CITY: Denver
; STATE: Colorado
; COUNTRY: U.S.A.
; ZIP: 80203
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS

```


Db 198 ETGYIKFIPKNKESFWOFFPEPEFTQSKY-----LMIYKDNELTDSNTSQIEVLYTT 250

RESULT 54
US-09-144-776B-6
; Sequence 6, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-144-776B-6

Query Match 23.7%; Score 293.5; DB 3; Length 266;
Best Local Similarity 32.8%; Pred. No. 7.4e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKXSELRNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 27 AESQPPKPELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNLADKYKDYVDFGANYYYQCYFVKKTNDINSHQTDKRTCKMYGG 144
QY 111 VTLHDNNRLTEEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGY 170
Db 145 VTEHNGNQLDKYRSITVRVPEDGK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKCLY 202
QY 171 NSDSFGGKVGQGLIVHSSSEGSTVSVDLPDAQOQ--YPTDLLRIYRDNKKTINSENHLIDL 228
Db 203 EFN--SPYETGYIKFTIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNVDSKDVKIEV 259
QY 229 YLYT 232

Db 260 YLYT 263
RESULT 55
US-08-882-431B-6
; Sequence 6, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-08-882-431B-6

Query Match 23.7%; Score 293.5; DB 4; Length 266;
Best Local Similarity 32.8%; Pred. No. 7.4e-22;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKXSELRNLSNRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
Db 27 AESQPPKPELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVGLSKDATNKYKGGKVDLYGAYYGYQC-----AGGTPNKTCMYGG 110
Db 85 LGDYDNVRVEFKNLADKYKDYVDFGANYYYQCYFVKKTNDINSHQTDKRTCKMYGG 144
QY 111 VTLHDNNRLTEEEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGY 170
Db 145 VTEHNGNQLDKYRSITVRVPEDGK-NLLSPD-VQTNKKKVTAGELDYLTRHYLVKNKCLY 202
QY 171 NSDSFGGKVGQGLIVHSSSEGSTVSVDLPDAQOQ--YPTDLLRIYRDNKKTINSENHLIDL 228
Db 203 EFN--SPYETGYIKFTIENENS-FWYDMPAPGDKFAQSKYLMYNDNKNVDSKDVKIEV 259
QY 229 YLYT 232
Db 260 YLYT 263

```
RESULT 56
US-08-896-933-26
; Sequence 26, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-08-896-933-26

Query Match      23.6%; Score 292.5; DB 3; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

Qy  2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
Db  1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy  62 PWYNDLLVGLSKDATNKYKGKVDLYGAYGYOC-----AGGTPNKTCMYGGV 111
Db  59 GYDNRVVEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGGV 118
Qy  112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db  119 TEHNGNQLDKYRSLTRVVFEDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy  172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
Db  177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDSDVKVIEVY 233
Qy  230 L 230
Db  234 L 234

RESULT 57
US-09-314-235-26
; Sequence 26, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0

Query Match      23.6%; Score 292.5; DB 3; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

Qy  2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
Db  1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy  62 PWYNDLLVGLSKDATNKYKGKVDLYGAYGYOC-----AGGTPNKTCMYGGV 111
Db  59 GYDNRVVEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGGV 118
Qy  112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db  119 TEHNGNQLDKYRSLTRVVFEDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy  172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
Db  177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDSDVKVIEVY 233
Qy  230 L 230
Db  234 L 234

RESULT 58
US-09-708-008B-26
; Sequence 26, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 26
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-26

Query Match      23.6%; Score 292.5; DB 4; Length 239;
Best Local Similarity 34.0%; Pred. No. 8e-22;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

Qy  2 EKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTGH 61
Db  1 ESQDPKPELHKSKF-TGLMNMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy  62 PWYNDLLVGLSKDATNKYKGKVDLYGAYGYOC-----AGGTPNKTCMYGGV 111
Db  59 GYDNRVVEFNKDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCTMYGGV 118
Qy  112 TLHDNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db  119 TEHNGNQLDKYRSLTRVVFEDGK-NLLSFD-VQTNKKKVTAAQELDYLTRHYLVKNKKLYE 176
Qy  172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENLIHDLY 229
Db  177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMYNDNKNKVDSDVKVIEVY 233
Qy  230 L 230
Db  234 L 234
```

```
QY 230 L 230
|
Db 234 L 234

RESULT 59
US-09-414-276-8
; Sequence 8, Application US/09414276
; Patent No. 6392121
; GENERAL INFORMATION:
; APPLICANT: Mason, Hugh
; APPLICANT: Palmer, Kenneth
; APPLICANT: Hefferon, Kathleen
; APPLICANT: Mor, Taafir
; APPLICANT: Arntzen, Charles
; TITLE OF INVENTION: Gemini Virus Vectors for Gene Expression in Plants
; FILE REFERENCE: 4868/84453
; CURRENT APPLICATION NUMBER: US/09/414,276
; CURRENT FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 8
; LENGTH: 266
; TYPE: PRT
; ORGANISM: bean yellow dwarf virus
US-09-414-276-8

Query Match 23.6%; Score 292.5; DB 3; Length 266;
Best Local Similarity 33.2%; Pred. No. 9.4e-22;
Matches 81; Conservative 47; Mismatches 97; Indels 19; Gaps 8;

QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 27 AESQDPKDELHKSCKP-TGLMENKVLDDNHVSAT-NVKSIDQSLYDFDIYSIKDTK 84
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 61 HPWYNDLLVLDGSKOATNKYKGGVDLYGAYGYQC-----AGTTPNKTAQMYGG 110
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 85 LGYDNRVVEFNKDLADKYKVDVFCANYYQCYFSKKTNDINSHQTDKRTKTCMYGG 144
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 111 VTLHNNRLTEKKVPINLWIDGKQTTVIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 145 VTEHNGNQLDKYRSITRVFEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNNKLY 202
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 171 NSDSFGKVGQGLIVFHSSEGSVSYVDLDAQOQYD--TLRIYRDNKTINSENHLIDL 228
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 203 EFN--SPYETGVKFIENENS-FWYDMPAPGDKFDQSKYLMYNDNKQVSKDVKIEV 259
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 229 YLYT 232
| |
Db 260 YLTT 263

RESULT 60
US-08-973-391C-14
; Sequence 14, Application US/08973391C
; Patent No. 6632441
; GENERAL INFORMATION:
; APPLICANT: Schlievert, Patrick M.
; APPLICANT: Roggiani, Manuela
; APPLICANT: Stoehr, Jennifer
; APPLICANT: Ohlendorf, Douglas
; TITLE OF INVENTION: MUTANTS OF STREPTOCOCCAL TOXIN A AND METHODS OF USE
; FILE REFERENCE: 600.311USWO
; CURRENT APPLICATION NUMBER: US/08/973,391C
; CURRENT FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: PCT/US96/10252
; PRIOR FILING DATE: 1996-06-07
; PRIOR APPLICATION NUMBER: US 08/480,261
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 14

; LENGTH: 221
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-973-391C-14

Query Match 23.5%; Score 291.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 9.1e-22;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;

QY 16 SELQNAL-SNLRQIYY-YNKAIT-ENKESDDQFLENTLLFKGFFTGHPWYNDLLVDIG 72
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 7 SOLHSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLYN---VSGPNYDKLKLTELK 63
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 73 SKDATNKYKGGVDLYGAYGYQC-AGTTPNKTAQMYGVTLHNNRLTEKKVPINLWI 131
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 64 NQEWATLFDKRNVDIYGVYHLCYLCENABRSACIYGGVTNHEGNHLEIPKKIYVVKVSI 123
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 132 DGKQTTVIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEG 191
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 124 DGIQ-SLSFD-IETNKKQWTAQELDYKVKYLTDNKQLYTNGP--SKYETGYIKFIPKNK 179
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 192 STVSYDLFD---AQOQYPTLLRIYRDNKTINSENHLIDLXYLT 232
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 180 ESFWEDEFFPEFTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220
| : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 61
US-09-144-776B-16
; Sequence 16, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MPMC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 16:
```

US-09-144-776B-16

Query Match 23.4%; Score 289.5; DB 3; Length 251;
Best Local Similarity 33.8%; Pred. No. 1.8e-21;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;
Qy 4 SEEINEKDLRKSELRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGPFPTG 60
Db 25 SQEFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81
Qy 61 HPWNLDLVLSGSKDATNKYKGVVDLYGAYGYQC-AGGTPNKTACMGYGVTHLDNNRL 119
Db 82 GPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHL 141
Qy 120 TEEKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKWTAQELDYKVRKYLTDNKQLTYNGP--SKY 197
Qy 180 QRLVIFHSSSEGSTVSYDLFD----AQQYPTDLLRIYRDNKTINSENHLIDLXYLT 232
Db 198 ETGYIKFIPKNKESFWDFPPEPFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250
RESULT 62
US-08-882-431B-16
; Sequence 16, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 251
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-16

Query Match 23.4%; Score 289.5; DB 4; Length 251;
Best Local Similarity 33.8%; Pred. No. 1.8e-21;
Matches 80; Conservative 45; Mismatches 93; Indels 19; Gaps 10;

Qy 4 SEEINEKDLRKSELRNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGPFPTG 60
Db 25 SQEFAQQDDPSPQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDLRSHDLIYN--VS 81
Qy 61 HPWNLDLVLSGSKDATNKYKGVVDLYGAYGYQC-AGGTPNKTACMGYGVTHLDNNRL 119
Db 82 GPNYDKLTKELKNQEMATLFDKNVDIYGVYHLCYLCEAERSACIYGGVTNHEGNHL 141
Qy 120 TEEKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLOARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKIVVKSIDGIQ-SLSFD-IETNKKWTAQELDYKVRKYLTDNKQLTYNGP--SKY 197
Qy 180 QRLVIFHSSSEGSTVSYDLFD----AQQYPTDLLRIYRDNKTINSENHLIDLXYLT 232
Db 198 ETGYIKFIPKNKESFWDFPPEPFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 63
US-09-144-776B-10
; Sequence 10, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 239
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-144-776B-10

Query Match 23.3%; Score 288.5; DB 3; Length 239;
Best Local Similarity 33.9%; Pred. No. 2.1e-21;
Matches 80; Conservative 45; Mismatches 88; Indels 23; Gaps 8;

Qy 14 KXSELRNA-----LSNLRQIYYNEKAITENKESDDQFLENTLLFKGPFTHWYNDLL 68
Db 7 KPDELHKSXKFTGLMENNKVLYDDNHSVSAI-NVKSIDQFRYFDLIYSIKDKLGNYNVR 65

RESULT 65
US-09-144-776B-8
; Sequence 8, Application US/09144776B
; Patent No. 6399332

```
Query Match      22.8%; Score 282.5; DB 3; Length 266;  
Best Local Similarity 32.8%; Pred. No. 1e-20;  
Matches 80; Conservative 46; Mismatches 99; Indels 19; Gaps 8;
```

Qy 1 SEKSEETNEKDRLKRSLQRNALSNLRQIYYNKEAITENKESDDDFLENTLLFKGFTTG 60

[illegible]

Qy 171 NSDSFGGKVGQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMWVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263

RESULT 66
US-08-882-431B-8
; Sequence 8, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882.431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-8

Query Match 22.8%; Score 282.5; DB 4; Length 266;
Best Local Similarity 32.8%; Pred. No. 1e-20; 99; Indels 19; Gaps 8;
Matches 80; Conservative 46; Mismatches 99; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQDPKPDLELHKSXF-TGLMENMKVLYDDNHVSAI-NVKSIDQPRYFDLIYSIKDTK 84
Qy 61 HPWYNDLLVDLGSVDATNKYKGVLDLYGAYGYQCAGG-----TENKTCMYGG 110
Db 85 LGNYDNVRVFEKNDLADKYDKYDVFEGANAYYQCAFSEKNTDINSHQTDKRTKCYGG 144
Qy 111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHLHGKFGELY 170
Db 145 VTEHNGQLDKVRSITVRVFEDEK-NLLSFD-VQVKKKVTQAQELDYLTRHLVKNKKLY 202
Qy 171 NSDSFGGKVGQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 228

Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMWVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263

RESULT 67
US-08-896-933-28
; Sequence 28, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896.933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252.978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-08-896-933-28

Query Match 22.7%; Score 281.5; DB 3; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;
Qy 11 DLRKXSELQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69
Db 9 ELHKSSEF-TGTMCNMK--LYDDHYVSATKVMVDKFLAHDLIYNTSDKKLKNYDKVKTK 65
Qy 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGTTPNKTCMYGGVTLHDNNRLTEE 122
Db 66 ELLNDELAKYKDEVVDYGSNYVNCYFSSKDNVKGVTGCKTCMYGGITKEGHNHFDNG 125
Qy 123 --KKVPINLWIDGKQTTVPIDKVKTSKEVTVQBELDQARHLHGKFGELYNDSFGGKVQ 180
Db 126 NLQNVLRVY-ENKRNITISPE-VQTDKKSVTQAQELDIKARNFLINKNLYSFNS--SPYE 181
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLIRIYRONKNTINSENHLIDL 232
Db 182 TGYIKFIENNGNTFWYDLMFAPGDKFDQSKYLMYNDNMWVDSKSVKIEVHLTT 235

RESULT 68
US-09-314-235-28
; Sequence 28, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314.235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896.933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252.978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891.718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466.577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416.530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34

```

US-08-896-933-27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-314-235-28
Query Match      22.7%; Score 281.5; DB 3; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELQNALSLNRIQYYNEKAITENK-ESDDQFLENTLFPKGFTHGWYNDLLV 69
DB 9 ELHKSEPT-TGTGNK--YLDDHVVSATKMSVDKFLAHDLIYNSDKKLKNYDKVKT 65
QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKATACMYGVTLDHNNRLTEE 122
DB 66 ELLNEDLAKKYDEVVDVYGSNYVNCYFSSKDNVGVTKGCTCMYGGITKHEGNHFDNG 125
QY 123 --KKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 126 NLQNVLIIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKKNLYEFNS--SPYE 181
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLDLYLT 232
DB 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLT 235

RESULT 69
US-09-708-008B-28
; Sequence 28, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-28
Query Match      22.7%; Score 281.5; DB 4; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELQNALSLNRIQYYNEKAITENK-ESDDQFLENTLFPKGFTHGWYNDLLV 69
DB 9 ELHKSEPT-TGTGNK--YLDDHVVSATKMSVDKFLAHDLIYNSDKKLKNYDKVKT 65
QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKATACMYGVTLDHNNRLTEE 122
DB 66 ELLNEDLAKKYDEVVDVYGSNYVNCYFSSKDNVGVTKGCTCMYGGITKHEGNHFDNG 125
QY 123 --KKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 126 NLQNVLIIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKKNLYEFNS--SPYE 181
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLDLYLT 232
DB 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLT 235

RESULT 70
US-09-708-008B-28
; Sequence 28, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 28
; LENGTH: 238
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-09-708-008B-28
Query Match      22.7%; Score 281.5; DB 4; Length 238;
Best Local Similarity 32.5%; Pred. No. 1.1e-20;
Matches 76; Conservative 47; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLKKSSELQNALSLNRIQYYNEKAITENK-ESDDQFLENTLFPKGFTHGWYNDLLV 69
DB 9 ELHKSEPT-TGTGNK--YLDDHVVSATKMSVDKFLAHDLIYNSDKKLKNYDKVKT 65
QY 70 DLGSKDATNKYGGKVDLYGAYGYQC-----AGGTPNKATACMYGVTLDHNNRLTEE 122
DB 66 ELLNEDLAKKYDEVVDVYGSNYVNCYFSSKDNVGVTKGCTCMYGGITKHEGNHFDNG 125
QY 123 --KKVPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
DB 126 NLQNVLIIRVY-ENKRNITISFE-VQTDKKSVAQELDIKARNFLINKKNLYEFNS--SPYE 181
QY 181 RGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKTINSENHLDLYLT 232
DB 182 TGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHLT 235

RESULT 71
US-09-314-235-27
; Sequence 27, Application US/09314235
; Patent No. 633845
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT

```

```
; ORGANISM: Staphylococcus aureas
US-09-314-235-27

Query Match      21.6%; Score 267.5; DB 3; Length 239;
Best Local Similarity 31.0%; Pred. No. 2.9e-19;
Matches 75; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

Qy 2 EKSEINEKDLRKSELQNALSLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ESQDPTDELHKASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFLAHDLIYNSDKKL 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYOC-----AGGTPNKTCMYGGVTLH 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 KNYDKVKTELLNEGLAKKYDEVVDVYGSNNYVNCYFSSKDNVKGVTGGTKTCMYGGITKH 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNS 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 EGNHFDNGNLQNVLRVY-ENKRNITISFE-VQTKKSVTAQELDIKARNFLINKNLYEF 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 173 DSFGGKVGQRLIVFHSSEGSTVSVDLPDAQOQYDP--TLRLIYRDNKTINSENLHIDL 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 NS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHL 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 231 YT 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 TT 236

RESULT 72
US-09-708-008B-27
; Sequence 27, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Tetman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708.008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896.933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252.978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 27
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Staphylococcus aureas
US-09-708-008B-27

Query Match      21.6%; Score 267.5; DB 4; Length 239;
Best Local Similarity 31.0%; Pred. No. 2.9e-19;
Matches 75; Conservative 49; Mismatches 101; Indels 17; Gaps 8;

Qy 2 EKSEINEKDLRKSELQNALSLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ESQDPTDELHKASKF-TGLMENMKVLYDDHYVSATKVK-SVDKFLAHDLIYNSDKKL 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYOC-----AGGTPNKTCMYGGVTLH 114
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 KNYDKVKTELLNEGLAKKYDEVVDVYGSNNYVNCYFSSKDNVKGVTGGTKTCMYGGITKH 118
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 115 DNNRLTEE--KKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGLYNS 172
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 119 EGNHFDNGNLQNVLRVY-ENKRNITISFE-VQTKKSVTAQELDIKARNFLINKNLYEF 176
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 173 DSFGGKVGQRLIVFHSSEGSTVSVDLPDAQOQYDP--TLRLIYRDNKTINSENLHIDL 230
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 177 NS--SPYETGYIKFIENNGNTFWYDLMPAPGDKFDQSKYLMYNDNKTVDKSKVIEVHL 234
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 231 YT 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 235 TT 236
```

```
; ORGANISM: Staphylococcus aureas
US-09-314-235-21

Query Match      21.0%; Score 260.5; DB 3; Length 239;
Best Local Similarity 31.8%; Pred. No. 1.5e-18;
Matches 78; Conservative 47; Mismatches 97; Indels 23; Gaps 10;

Qy 2 EKSEINEKDLRKSELQNALSLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 1 ESQDPTDELHKASKF--TGLMENMKVLYNDHVSAINVKSINEFFDLIYLSIKDTKL 58
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 62 PWYNDLLVGLSGKDATNKYKGGKVDLYGAYGYOC-----AGGTPNKTCMYGG 110
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 59 GNYDNVRFVEFKNDLADKYDYDVFGANV-YQCYFSKKTNNIDSHENTKRKT-CMYGG 116
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 111 VTLDHNNRLTE-EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFG 169
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 117 VTEHGNQLDKYRSITVRVFEDGK-NLLSFD-VQTNKKKVTAEQLDYLTHYLVKNKL 174
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 170 YNSDSFGGKVGQRLIVFHSSEGSTVSVDLPDAQOQYDP--TLRLIYRDNKTINSENLH 227
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 175 YEFNN--SPYETGYIKFIENENS-FWYDMPAPGNKFDQSKYLMYNDNKTVDKSKV 231
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Qy 228 LYLYT 232
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 232 VYLT 236

RESULT 74
US-09-314-235-21
; Sequence 21, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Tetman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314.235
; CURRENT FILING DATE: 1999-03-18
; EARLIER APPLICATION NUMBER: 08/896.933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252.978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891.718
; EARLIER FILING DATE: 1992-08-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466.577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416.530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
```


Db 203 FNS--SFYETGYIKFIENNGNTFWYDMMAPGDKPFDQSKYLMYNDKNTVDSKSVKIEVH 260
Qy 230 LYT 232
Db 261 LTT 263

RESULT 77
US-08-882-431B-14
; Sequence 14, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 266
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-14

Query Match 20.9%; Score 258.5; DB 4; Length 266;
Best Local Similarity 30.0%; Pred. No. 2.9e-18;
Matches 73; Conservative 51; Mismatches 102; Indels 17; Gaps 8;

Qy 1 SEKSEINEKDLRKKSELQNALSNLRQIYYNYNEKAITENKESDDQFLENTLLFKGFTTG 60
Db 27 AESQPDPTPDELHKASKF-TGLMENMKVLYDDHYVVSATKVK-SVDKFRADLIYINISDKK 84
Qy 61 HPWYNDLLDLGSDATNKYKGGKVDLYGAYVGYOC-----AGGTENKTACMYGGVTL 113
Db 85 LKNYDKVKVTELLNEGLAKYKDEVDVYGSNYNYNCYFSSKDNVGVKVTGGKTCMYGGITK 144
Qy 114 HDNRLTTEE--KKVPINLWIDGKQTPIDPKVTKTSKEVTVQELDLQARHYLHGKFGLYN 171
Db 145 HEGNHFDNGNLQNLVIRVY-ENKRNITISFE-VQTDKKSVTQAQELDIKARNFLINKNLYE 202
Qy 172 SDSFGGKVQGLIIVPHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNKTINSENLHIDL 229
Db 203 FNS--SFYETGYIKFIENNGNTFWYDMMAPGDKPFDQSKYLMYNDKNTVDSKSVKIEVH 260

Qy 230 LYT 232
Db 261 LTT 263

RESULT 78
US-08-896-933-20
; Sequence 20, Application US/08896933
; Patent No. 6221351
; GENERAL INFORMATION:
; APPLICANT: Tetman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/08/896,933
; CURRENT FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-08-896-933-20

Query Match 19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

Qy 14 KKSLEQNALSNLRQIYYNYNEKA--IT-ENKESDDQFLENTLLFKGFTGHPWYNDLLVD 70
Db 5 KPSQLQRSNLVKTPIYIFFMRVTLVTHENVKSVQDQLLSDLIYN---VSGPNYDKLAKTE 61
Qy 71 LGSKDATNKYKGGKVDLYGAYVGYOC-AGTNPNTACMYGVTJHDNRLTTEEKKVPINL 129
Db 62 LKNQEMATLFDKKNVDIYGVVYHLCYLCAEASACLYGCVTNHEGHNHLEIPKKIVVKV 121
Qy 130 WIDGKQT-TVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQGLIIVPHS 188
Db 122 SIDGIQSLSFDEIQIKNG----NCSRIYTVRKVLTNKNQLYTNGP--SKYETGYIKFIP 175
Qy 189 SEGSTVSVDLFD-----AQGGVPTDLLRIYRDNKTINSENLHIDL 232
Db 176 KNKESFWDFPPEPEFTQSKY----LMYKDNETLDSNTSQIEVYLT 219

RESULT 79
US-09-314-235-20
; Sequence 20, Application US/09314235
; Patent No. 6338845
; GENERAL INFORMATION:
; APPLICANT: Tetman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; TITLE OF INVENTION: SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005004
; CURRENT APPLICATION NUMBER: US/09/314,235
; CURRENT FILING DATE: 1999-05-18
; EARLIER APPLICATION NUMBER: 08/896,933
; EARLIER FILING DATE: 1997-07-18
; EARLIER APPLICATION NUMBER: 08/252,978
; EARLIER FILING DATE: 1994-06-02
; EARLIER APPLICATION NUMBER: 07/891,718
; EARLIER FILING DATE: 1992-06-01
; EARLIER APPLICATION NUMBER: US91/00342
; EARLIER FILING DATE: 1991-01-17
; EARLIER APPLICATION NUMBER: 07/466,577
; EARLIER FILING DATE: 1990-01-17
; EARLIER APPLICATION NUMBER: 07/416,530
; EARLIER FILING DATE: 1989-10-03
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSEQ for Windows Version 3.0

```
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-314-235-20

Query Match      19.8%; Score 245; DB 3; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKSELORNALSNLROIYYNEKA--IT-ENKESDDOFLNTLLFKGFTGHPWYNDLLVD 70
DB 5 KPSQLQSNLVTFKIYIPFMRVLTVTHENVKSDQLSHDLIYN---VSGPNYDKLKTE 61
QY 71 LGSKDATNKYGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINL 129
DB 62 LKQEMATLFDKKNVDIYGVYHLYCNCENASACLYGGVTNHEGNHLEIPKIVVKV 121
QY 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
DB 122 SIDGIQSLSFDEIQKNG---NCSRSIVTVRKYLTDNKLTYNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSYDLFD-----AQQYPTLLRIYRDNKTINSENHLIDLYLT 232
DB 176 KKNESFWDFEPPPEFTOSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 80
US-09-708-008B-20
; Sequence 20, Application US/09708008B
; Patent No. 6692746
; GENERAL INFORMATION:
; APPLICANT: Terman, David S.
; TITLE OF INVENTION: TUMOR KILLING EFFECTS OF ENTEROTOXINS,
; SUPERANTIGENS, AND RELATED COMPOUNDS
; FILE REFERENCE: 09629/005002
; CURRENT APPLICATION NUMBER: US/09/708,008B
; CURRENT FILING DATE: 2000-11-08
; PRIOR APPLICATION NUMBER: US/08/896,933
; PRIOR FILING DATE: 1997-07-18
; PRIOR APPLICATION NUMBER: 08/252,978
; PRIOR FILING DATE: 1994-06-02
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 20
; LENGTH: 220
; TYPE: PRT
; ORGANISM: Streptococcus pyogenes
US-09-708-008B-20

Query Match      19.8%; Score 245; DB 4; Length 220;
Best Local Similarity 30.7%; Pred. No. 5.3e-17;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKSELORNALSNLROIYYNEKA--IT-ENKESDDOFLNTLLFKGFTGHPWYNDLLVD 70
DB 5 KPSQLQSNLVTFKIYIPFMRVLTVTHENVKSDQLSHDLIYN---VSGPNYDKLKTE 61
QY 71 LGSKDATNKYGGKVDLYGAYGYQC--AGGTPNKTCMYGGVTLHDNNRLTEKKVPINL 129
DB 62 LKQEMATLFDKKNVDIYGVYHLYCNCENASACLYGGVTNHEGNHLEIPKIVVKV 121
QY 130 WIDGKQT-TVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHS 188
DB 122 SIDGIQSLSFDEIQKNG---NCSRSIVTVRKYLTDNKLTYNGP--SKYETGYIKFIP 175
QY 189 SEGSTVSYDLFD-----AQQYPTLLRIYRDNKTINSENHLIDLYLT 232
DB 176 KKNESFWDFEPPPEFTOSKY----LMIYKDNETLDSNTSQIEVYLTT 219

RESULT 81
US-09-144-776B-18
```

```
; Sequence 18, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MEMC -504 Scott Street
; MCMR-JA (Charles H. Harris-Patent
; Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-144-776B-18

Query Match      17.4%; Score 215; DB 3; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.5e-14;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

QY 45 DOFLENTLLFKGFTGHPWYNDLLVGLSKDATNKYGGKVDLYGAYGYQCAGGTPNKT 104
DB 3 DOFLENTLLYKFFDTDLINFEDLLINFNSKEMAQHFKSNVDVYPIRYINCYGGIDRT 62
QY 105 ACMYGGVTLHDNNRLTEKK 124
DB 63 ACTYGGVTPHEGNKLERKK 82

RESULT 82
US-08-882-431B-18
; Sequence 18, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
```

```
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Att'y)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882.431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 82
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-18

Query Match 17.4%; Score 215; DB 4; Length 82;
Best Local Similarity 51.2%; Pred. No. 1.5e-14;
Matches 41; Conservative 11; Mismatches 28; Indels 0; Gaps 0;

Qy 45 DQLENTLLFGFFTHGHPWYNDLLVLSKDATNKYKGGKYDLYGAYYGOCAGTPTNKT 104
Db 3 DQLENTLLYKFFDTDLINFDLLINFNSKEWAQHFKSKNDVPIRYINCYGGEIDRT 62

Qy 105 ACMYGGVTLHDNNRLTEKK 124
Db 63 ACTYGGVTPHEGNLKERKK 82

RESULT 83
US-08-220-378-1
; Sequence 1, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220.378
; FILING DATE: 29-MAR-1994
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; CLASSIFICATION: 530
```

```
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-220-378-1

Query Match 15.4%; Score 191; DB 1; Length 45;
Best Local Similarity 86.7%; Pred. No. 1.8e-12;
Matches 39; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKXSELQNALNSLRQIYYYNKAITENKESDD 45
Db 1 SEKSEINEKDLRKXSELQGTALGNLQIYYYNKAKTENKESHD 45

RESULT 84
US-08-696-012-1
; Sequence 1, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 45 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
```


;
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-09-144-776B-20

Query Match 11.1%; Score 137.5; DB 3; Length 89;
Best Local Similarity 39.1%; Pred. No. 1.5e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQPLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC----- 96
Db 1 SIDQFLYFDLYSIKDTKLGNDVNRVFEKKNLADKYDKYDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTYACMYGGVTLHDNNRL 119
Db 60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86

RESULT 91
US-08-882-431B-20
; Sequence 20, Application US/08882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; APPLICANT: Mark A. Olson
; APPLICANT: Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; TITLE OF INVENTION: Vaccines
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street MCMR-JA (Charles H. Harris-Patent Atty)
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/0882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 89
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
US-08-882-431B-20

Query Match 11.1%; Score 137.5; DB 4; Length 89;
Best Local Similarity 39.1%; Pred. No. 1.5e-06;
Matches 34; Conservative 14; Mismatches 28; Indels 11; Gaps 2;

QY 43 SDDQPLENTLLFKGFTGHPWYNDLLVGLSKDATNKYKGGKVDLYGAYGYQC----- 96
Db 1 SIDQFLYFDLYSIKDTKLGNDVNRVFEKKNLADKYDKYDVFGANY-YQCYFSKKT 59

QY 97 ----AGGTPNKTYACMYGGVTLHDNNRL 119
Db 60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86

Db 60 NDINSHQTDKRKTCMYGGVTEHNGNQL 86

RESULT 92
US-08-378-2
; Sequence 2, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-220-378-2

Query Match 10.4%; Score 129; DB 1; Length 28;
Best Local Similarity 78.6%; Pred. No. 2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 39 ENKESDDQPLENTLLFKGFTGHPWYND 66
Db 1 ENKESDDQPLENTLLFKGFTGHPWYND 28

RESULT 93
US-08-696-012-2
; Sequence 2, Application US/08696012
; Patent No. 5859207
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville

```
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/696,012
; FILING DATE: 12-AUG-1996
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 2:
; LENGTH: 28 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-696-012-2

Query Match 10.4%; Score 129; DB 2; Length 28;
Best Local Similarity 78.6%; Pred. No. 2e-06;
Matches 22; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 39 ENKESDQFLENTLLFKGFFGTHPWYND 66
Db 1 ENKSHQFLQHTILFRGFFTHDHSWYND 28

RESULT 94
US-08-838-413A-22
; Sequence 22, Application US/08838413A
; Patent No. 6075119
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: PEPTIDES USEFUL FOR
; TITLE OF INVENTION: REDUCING SYMPTOMS OF TOXIC SHOCK SYNDROME
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WORDPERFECT 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/838.413A
; FILING DATE: 07-APR-1997
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; CLASSIFICATION: 536
```

```
; ATTORNEY/AGENT INFORMATION:
; NAME: MORRY, MARY J.
; REGISTRATION NUMBER: 34,398
; REFERENCE/DOCKET NUMBER: 2016-4010
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212)758-4800
; TELEFAX: (212)751-6849
; INFORMATION FOR SEQ ID NO: 22:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 24
; TYPE: AMINO ACID
; STRANDEDNESS: UNKNOWN
; TOPOLOGY: UNKNOWN
; MOLECULE TYPE: PEPTIDE
; US-08-838-413A-22

Query Match 10.3%; Score 127; DB 3; Length 24;
Best Local Similarity 100.0%; Pred. No. 2.6e-06;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 147 KKEVTVOELDLQARHYLHGKFGLY 170
Db 1 KKEVTVOELDLQARHYLHGKFGLY 24

RESULT 95
US-08-220-378-5
; Sequence 5, Application US/08220378
; Patent No. 5545716
; GENERAL INFORMATION:
; APPLICANT: Johnson, Howard M.
; APPLICANT: Pontzer, Carol H.
; APPLICANT: Griggs, Nathan D.
; TITLE OF INVENTION: Superantigen Agonist and Antagonist
; TITLE OF INVENTION: Peptides
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Saliwanchik & Saliwanchik
; STREET: 2421 N.W. 41st Street, Suite A-1
; CITY: Gainesville
; STATE: FL
; COUNTRY: USA
; ZIP: 32606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/220,378
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UF126.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 23 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-220-378-5

Query Match 10.2%; Score 126; DB 1; Length 23;
Best Local Similarity 100.0%; Pred. No. 3.1e-06;
```


1

```
;
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/220,378
; FILING DATE: 29-MAR-1994
; APPLICATION NUMBER: US 07/941,497
; FILING DATE: 08-SEP-1992
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Saliwanchik, David R.
; REGISTRATION NUMBER: 31,794
; REFERENCE/DOCKET NUMBER: UFI26.C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 904-375-8100
; TELEFAX: 904-372-5800
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 29 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-696-012-6

Query Match 10.0%; Score 124; DB 2; Length 29;
Best Local Similarity 78.6%; Pred. No. 7e-06;
Matches 22; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 121 BEKKVPINLWIDGQTTVPIDKVTSKK 148
Db 1 BEKKVPINLWIDGQNTVPLETVTNKK 28

RESULT 99
US-09-144-776B-24
; Sequence 24, Application US/09144776B
; Patent No. 6399332
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/144,776B
; FILING DATE: 01-Sep-1998
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/882,431
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER: <Unknown>
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 2; Conservative 15; Mismatches 32; Indels 4; Gaps 2;
```

```
;
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 24:
US-09-144-776B-24

Query Match 9.8%; Score 121; DB 3; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 27; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

Qy 43 SDDQFLENTLLFKGFTTGHFWNDLLVDLGSKDATNKYKGKVDLYGAYGYQC-AGGTP 101
Db 1 SVDQLLSDHLLYN---VSGPNYDKLTELKKNQENATLFDKKNVDIYGVEYVHLCVCENA 57
Qy 102 NKTACMYGGVTLHDNNRL 119
Db 58 ERSACIYGGVTNHEGNHL 75

RESULT 100
US-08-882-431B-24
; Sequence 24, Application US/0882431B
; Patent No. 6713284
; GENERAL INFORMATION:
; APPLICANT: Robert G. Ulrich,
; Mark A. Olson
; Sina Bavari
; TITLE OF INVENTION: Bacterial Superantigen
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles H. Harris
; STREET: US Army MRC -504 Scott Street
; CITY: FORT DETRICK
; STATE: MARYLAND
; COUNTRY: USA
; ZIP: 21702-5012
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 7.5
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/882,431B
; FILING DATE: June 25, 1997
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Charles H. Harris
; REGISTRATION NUMBER: 34,616
; REFERENCE/DOCKET NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 619-2065
; TELEFAX: (301) 619-7714
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-24

Query Match 9.8%; Score 121; DB 4; Length 79;
Best Local Similarity 34.6%; Pred. No. 6.1e-05;
Matches 2; Conservative 15; Mismatches 32; Indels 4; Gaps 2;

Qy 43 SDDQFLENTLLFKGFTTGHFWNDLLVDLGSKDATNKYKGKVDLYGAYGYQC-AGGTP 101
;
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 79
; TYPE: Amino Acid
; STRANDEDNESS: Unknown
; TOPOLOGY: Unknown
; MOLECULE TYPE: Peptide
; US-08-882-431B-24
```

Db 1 SVDQLLSDLIYN---VSGPNYDKLKTTELKNOEMATLFDKRNVDIYGVEYHLCYLCEA 57

Qy 102 NKTACMYGGVTLHDNNRL 119

Db :||:|||||:|
58 ERSACIYGGVTNHEGNHL 75

Search completed: July 26, 2005, 11:09:10
Job time : 28 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 10:57:03 ; Search time 72 Seconds
(without alignments)
1251.600 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKLRKSKSELQR.....RDNKTINSENLHLDLYLTT 233

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq.length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database : A_Geneseq_16Dec04:*

1: Genesecp1980s:*

2: Genesecp1990s:*

3: Genesecp2000s:*

4: Genesecp2001s:*

5: Genesecp2002s:*

6: Genesecp2003as:*

7: Genesecp2003bs:*

8: Genesecp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	233	6	Abp58456 Staphyloc
2	1238	100.0	257	4	Aau14103 Peptide s
3	1238	100.0	257	6	Abol10268 S. aureus
4	1238	100.0	257	8	Adf89830 Staphyloc
5	1234	98.9	230	4	Aab67339 Staphyloc
6	1222	98.7	245	2	Aaw35374 Staphyloc
7	1210	97.7	233	6	Abp58457 Engineer
8	1202	97.1	245	2	Aaw35375 Staphyloc
9	1188	96.0	248	6	Abu79072 S. aureus
10	1188	96.0	248	7	Adf43296 Staphyloc
11	1179	95.2	230	2	Aar45012 Staphyloc
12	1175	94.9	230	5	Abb76235 Staphyloc
13	1156	93.4	230	2	Aar13204 Staphyloc
14	1107	89.4	233	6	Abp58455 Engineer
15	1107	89.4	672	6	Abp58454 Engineer
16	1035	83.6	233	2	Aar13203 Staphyloc
17	1023	82.6	233	6	Abp58458 Staphyloc
18	1023	82.6	257	4	Aau14104 Peptide s
19	1023	82.6	257	6	Abol10269 S. aureus
20	1023	82.6	257	7	Ada44368 Staphyloc
21	1023	82.6	257	8	Adh10956 Enterotox
22	1019	82.3	233	2	Aaw06738 Staphyloc
23	1019	82.3	233	8	Adi95318 OSPF-rela
24	1016	82.1	233	2	Aaw35373 Staphyloc
25	1016	82.1	233	4	Aab67338 Staphyloc

26	1013	81.8	233	2	Aar45011 Staphyloc
27	1013	81.8	257	6	Abu79068 S. aureus
28	1013	81.8	257	7	Adf43288 Staphyloc
29	1004	81.1	233	5	Abb76234 Staphyloc
30	1000	80.8	257	5	Abb79501 Staphyloc
31	1000	80.8	257	6	Abu10081 Staphyloc
32	1000	80.8	257	7	Abu62324 S. aureus
33	1000	80.8	257	7	Abu62324 S. aureus
34	996	80.5	233	3	Aay54463 Amino aci
35	996	80.5	233	5	Abb79502 Staphyloc
36	996	80.5	233	6	Abu10082 Staphyloc
37	996	80.5	233	7	Abu62325 S. aureus
38	996	80.5	233	7	Aae37677 Protein #
39	992	80.1	233	6	Abu10099 Staphyloc
40	991	80.0	233	8	Adf89824 Staphyloc
41	987	79.7	233	6	Abu10098 Staphyloc
42	983	79.4	257	3	Aay70102 Staphyloc
43	978	79.0	233	3	Aay70103 Mutant St
44	830	67.0	268	8	Adf89835 Staphyloc
45	663	53.6	258	6	Abu79071 S. aureus
46	663	53.6	258	7	Adf43294 Staphyloc
47	663	53.6	258	8	Adf89829 Staphyloc
48	657	53.1	228	2	Aar45013 Staphyloc
49	657	53.1	228	4	Aab67340 Staphyloc
50	657	53.1	228	5	Abb76236 Staphyloc
51	649	52.4	228	2	Aar13205 Staphyloc
52	523	42.2	203	6	Abp58459 Staphyloc
53	492.5	39.8	250	6	Abm70958 Staphyloc
54	457	36.9	82	6	Abu10091 Bacterial
55	457	36.9	82	7	Abu62338 S. aureus
56	399	32.2	82	7	Abu10089 Bacterial
57	399	32.2	82	7	Abu62336 S. aureus
58	370	29.9	91	2	Aaw24299 Staphyloc
59	366	29.6	217	6	Abp58460 Staphyloc
60	366	29.6	217	8	Adf89833 Staphyloc
61	339.5	27.4	242	8	Adf89834 Staphyloc
62	337	27.2	240	8	Adf89837 Staphyloc
63	336.5	27.2	259	5	Abp29357 Streptoco
64	320	25.8	239	8	Adf89838 Staphyloc
65	319.5	25.8	242	8	Adf89832 Staphyloc
66	310	25.0	242	8	Adf89836 Staphyloc
67	300.5	24.3	266	6	Abu79069 S. aureus
68	300.5	24.3	266	7	Abg75015 S. aureus
69	300.5	24.3	266	7	Adf43290 Staphyloc
70	300	24.2	255	2	Aaw06737 Staphyloc
71	299.5	24.2	238	8	Adf89825 Staphyloc
72	299.5	24.2	239	2	Aaw64647 Synthetic
73	299.5	24.2	239	4	Aab67341 Staphyloc
74	299.5	24.2	239	7	Abg75016 Unidentifi
75	299.5	24.2	239	8	Adl14247 Wild type
76	297.5	24.0	251	2	Aaw12153 Streptoco
77	297.5	24.0	266	7	Abu62455 S. aureus
78	296.5	23.9	221	2	Aar13209 Streptoco
79	296.5	23.9	221	2	Aar45017 Staphyloc
80	296.5	23.9	221	5	Abb76240 Staphyloc
81	296.5	23.9	251	2	Aaw12151 Streptoco
82	295.5	23.9	251	2	Aaw12150 Streptoco
83	295.5	23.9	251	8	Adf89839 Streptoco
84	294.5	23.8	251	2	Aaw12154 Streptoco
85	294.5	23.8	251	2	Aaw12146 Streptoco
86	294.5	23.8	251	2	Aaw12097 Streptoco
87	294.5	23.8	251	2	Aaw12147 Streptoco
88	294.5	23.8	251	2	Aaw12148 Streptoco
89	294.5	23.8	251	2	Aaw59780 Amino aci
90	293.5	23.7	239	2	Aay06254 Staphyloc
91	293.5	23.7	240	6	Abg71370 Staphyloc
92	293.5	23.7	266	5	Abb79503 Staphyloc
93	293.5	23.7	266	6	Abu10083 Staphyloc
94	293.5	23.7	266	7	Abu62326 S. aureus
95	293.5	23.7	266	7	Aae37678 Protein #
96	292.5	23.6	221	4	Aab67344 Staphyloc
97	292.5	23.6	239	2	Aar13206 Staphyloc
98	292.5	23.6	239	2	Aar45014 Staphyloc

99	292.5	23.6	266	3	AA92319	Plant-opt	Aay92319	172	250	20.2	209	8	ADG69998	Adg69998	Mutant St
100	291.5	23.5	266	7	ABU62453	S. aureus	Abu62453	173	250	20.2	209	8	ADG70011	Adg70011	Mutant St
101	290.5	23.5	266	5	ABB76237	Staphyloc	Abb76237	174	247.5	20.0	209	8	ADG69999	Adg69999	Mutant St
102	290.5	23.5	251	7	ABU62460	Streptoco	Abu62460	175	247.5	20.0	209	8	ADG70010	Adg70010	Mutant St
103	289.5	23.4	251	2	AAW59798	Amino aci	Aaw59798	176	245.5	19.8	231	7	ADG64940	Adg64940	SEB pepti
104	289.5	23.4	251	2	AAW59781	Amino aci	Aaw59781	177	245	19.8	231	6	ABU79074	Abu79074	S. pyogen
105	289.5	23.4	251	3	AA770109	Streptoco	Aay770109	178	245	19.8	250	7	ADF43300	Adf43300	Pyrogenic
106	289.5	23.4	251	5	ABB79508	Streptoco	Abb79508	179	239	19.3	209	8	ADF89845	Adf89845	Streptoco
107	289.5	23.4	251	6	ABU10088	Streptoco	Abu10088	180	232	18.7	258	5	ABP29565	Abp29565	Streptoco
108	289.5	23.4	251	6	ABU62331	Streptoco	Abu62331	181	220.5	17.8	240	8	ADF89826	Adf89826	Staphyloc
109	289.5	23.4	251	7	AAE37683	Streptoco	Aae37683	182	217	17.5	234	3	AA93742	Aay93742	Amino aci
110	289.5	23.4	266	3	AA54464	Amino aci	Aay54464	183	217	17.5	234	5	ABP29092	Adp29092	Streptoco
111	288.5	23.3	239	2	AA54464	Staphyloc	Aay54464	184	216	17.4	210	8	ADF89843	Adf89843	Streptoco
112	288.5	23.3	239	5	AA706253	Staphyloc	Abb706253	185	215	17.4	82	6	ABU10090	Abu10090	Bacterial
113	288.5	23.3	239	6	ABB79505	Staphyloc	Abb79505	186	215	17.4	82	7	ABU62337	Abu62337	S. aureus
114	288.5	23.3	239	6	ABU10085	Staphyloc	Abu10085	187	197	15.9	236	3	AA93743	Aay93743	Amino aci
115	288.5	23.3	239	7	ABU62328	S. aureus	Abu62328	188	197	15.9	236	5	ABP29358	Abp29358	Streptoco
116	288.5	23.3	240	3	AA54465	Mutant St	Aay54465	189	197	15.9	236	8	ADF89844	Adf89844	Streptoco
117	288.5	23.3	240	6	ABG71369	Staphyloc	Abg71369	190	197	15.9	236	8	ADR83928	Adr83928	S. pyogen
118	287.5	23.2	239	2	AA706256	Staphyloc	Aay706256	191	193	15.6	232	5	ABP29143	Abp29143	Streptoco
119	287.5	23.2	239	3	AA770106	Mutant St	Aay770106	192	191	15.4	45	2	AAW04488	Aaw04488	Staphyloc
120	287.5	23.2	240	6	ABG71372	Staphyloc	Abg71372	193	191	15.4	45	2	AAW73917	Aaw73917	Staphyloc
121	287.5	23.2	266	7	ABU62454	S. aureus	Abu62454	194	185	14.9	234	8	ADF89841	Adf89841	Streptoco
122	285.5	23.1	239	2	AA706255	Staphyloc	Aay706255	195	183.5	14.8	235	2	AAW62788	Aaw62788	Mutant St
123	285.5	23.1	239	8	ADL14256	Modified	Adl14256	196	183.5	14.8	235	2	AAW62787	Aaw62787	Mutant St
124	285.5	23.1	240	6	ABG71371	Staphyloc	Abg71371	197	183.5	14.8	235	2	AAW62784	Aaw62784	Streptoco
125	285.5	23.1	266	8	ADF89828	Staphyloc	Adf89828	198	182.5	14.7	207	5	AAE25373	Aae25373	S. pyogen
126	284.5	23.0	251	2	AAW12149	Streptoco	Aaw12149	199	181.5	14.7	207	5	AAE25364	Aae25364	Streptoco
127	284.5	23.0	251	2	AAW12152	Streptoco	Aaw12152	200	181.5	14.7	208	2	AAE13210	Aae13210	Streptoco
128	284.5	23.0	266	7	ABU62452	S. aureus	Abu62452								
129	284.5	23.0	266	7	ABU62451	S. aureus	Abu62451								
130	283.5	22.9	239	2	AA706252	Staphyloc	Aay706252								
131	283.5	22.9	240	6	ABG71368	Staphyloc	Abg71368								
132	283	22.9	250	2	AAW12145	Streptoco	Aaw12145								
133	282.5	22.8	266	5	ABB79504	Staphyloc	Abb79504								
134	282.5	22.8	266	6	ABU10084	Staphyloc	Abu10084								
135	282.5	22.8	266	7	AAE37679	Protein #	Aae37679								
136	282.5	22.8	266	7	AAE37679	Staphyloc	Aae37679								
137	281.5	22.7	238	2	AA45016	Staphyloc	Aar45016								
138	280.5	22.7	239	8	ADF89827	Staphyloc	Adf89827								
139	280	22.6	265	3	AA770104	Staphyloc	Aay770104								
140	279.5	22.6	238	4	AAAB67343	Staphyloc	Aab67343								
141	279.5	22.6	238	5	ABB76239	Staphyloc	Abb76239								
142	276.5	22.3	228	4	AAAG63856	Amino aci	Aag63856								
143	276.5	22.3	238	2	AAAR13208	Staphyloc	Aar13208								
144	276.5	22.3	239	2	AA706258	Staphyloc	Aay706258								
145	276.5	22.3	239	2	AA706257	Staphyloc	Aay706257								
146	276.5	22.3	240	6	ABG71373	Staphyloc	Abg71373								
147	276.5	22.3	240	6	ABG71374	Staphyloc	Abg71374								
148	276	22.3	265	3	AA770105	Mutant St	Aay770105								
149	267.5	21.6	239	2	AAAR13207	Staphyloc	Aar13207								
150	267.5	21.6	239	2	AAAR45015	Staphyloc	Aar45015								
151	267.5	21.6	239	5	ABB76238	Staphyloc	Abb76238								
152	267.5	21.6	260	8	ADF89842	Streptoco	Adf89842								
153	266.5	21.5	266	7	ABU79070	S. aureus	Abu79070								
154	266.5	21.5	266	7	ADF43292	Staphyloc	Adf43292								
155	265.5	21.4	239	2	AA706251	Staphyloc	Aay706251								
156	265.5	21.4	239	4	AAAB67342	Staphyloc	Aab67342								
157	265.5	21.4	240	6	ABG71367	Staphyloc	Abg71367								
158	258.5	20.9	266	3	AA770108	Staphyloc	Aay770108								
159	258.5	20.9	266	5	ABB79507	Staphyloc	Abb79507								
160	258.5	20.9	266	6	ABU10087	Streptoco	Abu10087								
161	258.5	20.9	266	7	ABU62330	S. aureus	Abu62330								
162	258.5	20.9	266	7	AAE37682	Staphyloc	Aae37682								
163	256.5	20.7	220	7	ABU62334	Streptoco	Abu62334								
164	256.5	20.7	220	7	AAE37683	Streptoco	Aae37683								
165	256.5	20.7	468	7	ABU62335	SPEA L42R	Abu62335								
166	256.5	20.7	468	7	AAE37684	Streptoco	Aae37684								
167	256	20.7	209	8	ADG69997	Streptoco	Adg69997								
168	256	20.7	233	3	AA93741	Amino aci	Aay93741								
169	254.5	20.6	220	7	AAE37689	S. pyogen	Aae37689								
170	253.5	20.5	220	7	AAE37688	S. pyogen	Aae37688								
171	253.5	20.5	468	7	AAE37691	S. pyogen	Aae37691								

ALIGNMENTS

RESULT 1

ABP58456

ID ABP58456 standard; protein; 233 AA.

XX AC ABP58456;

XX DT 14-APR-2003 (first entry)

XX DE Staphylococcal enterotoxin E.

XX KW Superantigen; staphylococcal enterotoxin E; antibody; cancer; tumour;

XX KW Cytostatic; vaccine.

XX OS Staphylococcus sp.

XX FN WO2003002143-A1.

XX PD 09-JAN-2003.

XX XX 19-JUN-2002; 2002MO-SE001188.

XX XX 28-JUN-2001; 2001SE-00002327.

XX PA (ACTI-) ACTIVE BIOTECH AB.

XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;

XX DR WPI; 2003-201467/19.

XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX receptor and four regions to determine binding to class II major
XX histocompatibility complex, antibody to cancer associated cell surface
XX structure.

XX PS Example 3; Fig 4; 102pp; English.

XX CC The present sequence is the protein sequence of staphylococcal
XX enterotoxin SEB. The invention provides novel conjugates (see ABP58454)
XX for human cancer therapy. These comprise an engineered bacterial

CC superantigen, such as novel SEA/E-120 (see ABP58455), which is based on
CC SEE, and an antibody moiety, such as tumour reactive antibody 574. The
CC superantigen is engineered to reduce seroreactivity whilst maintaining
CC biological activity and production levels. The conjugates are designed to
CC target and destroy cancer cells, including cancer of the lung, breast
CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX
SQ Sequence 233 AA;

Query Match 100.0%; Score 1238; DB 6; Length 233;
Best Local Similarity 100.0%; Pred. No. 7e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 60
Db 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 60

Qy 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLVLTYTT 233
Db 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLVLTYTT 233

RESULT 2
AAU14103
ID AAU14103 standard; peptide; 257 AA.
XX AAU14103;
AC AAU14103;
DT 21-NOV-2001 (first entry)
DE Peptide sequence from Staphylococcus aureus enterotoxin type E.
XX Anti-retroviral; DP178-like; DP107-like; enterotoxin type E;
KW antifusogenic; antiviral; HIV transmission.
XX Staphylococcus aureus.
XX WO200151673-A2.
XX 19-JUL-2001.
XX 05-JUL-2000; 2000WO-US035727.
XX 09-JUL-1999; 99US-00350841.
XX (TRIM-) TRIMERIS INC.
XX Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX WPI; 2001-442157/47.
XX Identifying a compound that inhibits the formation of or disrupts a
PT DP107/DP178 complex, especially compounds with antifusogenic, antiviral
PT or intracellular modulatory activity, by detecting the formation of a
PT DP107/DP178 complex.
XX Disclosure; Fig 41; 259pp; English.

CC The present invention relates to peptides which exhibit anti-retroviral
CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
CC DP178-like and DP107-like peptides. The DP178 peptide corresponds to
CC amino acids 639-673 of the transmembrane protein gp41 from human
CC immunodeficiency virus 1 (HIV-1) isolate IAI. The DP107 peptide
CC corresponds to amino acids 558-595 of gp41 from HIV-1IAI. The invention
CC also relates to a method of identifying compounds that inhibit the

CC formation of or disrupts a DP107/DP178 complex. The method comprises
CC detecting the formation of a DP107/DP178 complex, both in the presence or
CC absence of a test compound, in a reaction mixture containing DP107 and
CC DP178 peptides. The method is useful for identifying compounds, including
CC small molecule compounds, which may themselves exhibit antifusogenic,
CC antiviral or intracellular modulatory activity. The DP178-like/DP107-like
CC peptides are useful to inhibit human and non-human retroviral,
CC particularly HIV, transmission to uninfected cells. The present sequence
CC represents a peptide sequence from Staphylococcus aureus enterotoxin type
XX E
SQ Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 60
Db 25 SEKSEINEKDLRKSEIQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFPTG 84

Qy 61 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVLDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTKACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLVLTYTT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSNLHIDLVLTYTT 257

RESULT 3
ABO10268
ID ABO10268 standard; protein; 257 AA.
XX ABO10268;
AC ABO10268;
DT 19-AUG-2003 (first entry)
XX S. aureus enterotoxin E.
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
KW Epstein-Barr virus infection; heptad repeat motif.
XX Staphylococcus aureus.
XX OS Staphylococcus aureus.
XX US6518013-B1.
XX 11-FEB-2003.
XX 07-JUN-1995; 95US-00485546.
XX 07-JUN-1993; 93US-00073028.
XX 07-JUN-1994; 94US-00255208.
XX 20-DEC-1994; 94US-00360107.
XX (TRIM-) TRIMERIS INC.
XX Barney SO, Lambert DM, Petteway SR;
XX WPI; 2003-465599/44.
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
PT the cell with a peptide consisting of a region of Epstein-Barr virus
PT protein.
XX Example; Fig 41; 716pp; English.
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
CC virus to a cell, comprising contacting the cell with an effective

concentration of a peptide consisting of a region of 16-39 consecutive amino acids of an Epstein-Barr virus protein for an effective period of time, where the region is recognised by one or more of ALLMOTIS, 107x178x4 or PL2IP sequence search motifs, the peptide further comprises an amino terminal X, and a carboxy terminal Z in which X comprises an amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic group or macromolecular carrier group, and Z comprises a carboxyl group, amido group, hydrophobic group, or macromolecular carrier group, and fusion of the virus to the cell is inhibited. The peptides were identified by analysing the structure/motifs present in the HIV-1 glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat motif containing peptides were used to design the motifs cited above, which in turn were used to analyse proteins from other pathogenic organisms and HIV isolates, looking for DP107/178 structural analogues. The method is useful for inhibiting transmission of Epstein-Barr virus to a cell and Epstein-Barr virus infection. The present sequence is a protein from a pathogenic organism analysed for regions analogous to DP107 or DP178

XX Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 6; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEENEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Dd 25 SEKSEENEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 84

Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Dd 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Dd 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 233
Dd 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 257

RESULT 4
ADF89830
ID ADF89830 standard; protein; 257 AA.
XX ADF89830;
XX
XX 26-FEB-2004 (first entry)
XX
XX Staphylococcal enterotoxin E (SEE) superantigen.
XX
XX Superantigen; SAg; Staphylococcal enterotoxin; SE; SEE; cytostatic;
KW gene therapy; cancer.
XX
XX Staphylococcus sp.
XX
XX WO2003094846-A2.
XX
XX 20-NOV-2003.
XX
XX 08-MAY-2003; 2003WO-US014381.
XX
XX 08-MAY-2002; 2002US-0378988P.
XX
XX 15-JUN-2002; 2002US-0389366P.
XX
XX 28-AUG-2002; 2002US-0406697P.
XX
XX 29-AUG-2002; 2002US-0406750P.
XX
XX 01-OCT-2002; 2002US-0415310P.
XX
XX 02-OCT-2002; 2002US-0415400P.
XX
XX 09-JAN-2003; 2003US-0438686P.
XX
XX (TERM/) TERMAN D S.

PI Terman DS;
XX
XX WPI; 2004-011997/01.
XX
XX Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
XX a superantigen composition to the subject.
XX
XX Disclosure; SEQ ID NO 7; 91pp; English.
XX
XX The invention relates to treating a subject with cancer. The method
XX involves administering an amount of a superantigen (SAG) composition
XX comprising a molecule selected from: a native SAG protein; its
XX biologically active fragment or a biologically active homologue or a
XX biologically active fusion protein comprising the SAG or its fragment or
XX homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
XX Clostridium perfringens exotoxin. The method is useful in treating cancer
XX or malignant diseases such as malignant pleural effusion, ascites,
XX pericardial effusion or meningeal carcinomatosis. The present sequence
XX represents a Staphylococcal enterotoxin E (SEE) superantigen.
XX
XX Sequence 257 AA;

Query Match 100.0%; Score 1238; DB 8; Length 257;
Best Local Similarity 100.0%; Pred. No. 8.1e-116;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 SEKSEENEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Dd 25 SEKSEENEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 84

Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 120
Dd 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMYGGVTLHDNNRLT 144

Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Dd 145 EEKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204

Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 233
Dd 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLHIDLILYTT 257

RESULT 5
AAB67339
ID AAB67339 standard; peptide; 230 AA.
XX AAB67339;
XX
XX 23-APR-2001 (first entry)
XX
XX Staphylococcus aureus enterotoxin E protein.
XX
XX Tumour; cancer; immune; enterotoxin.
XX
XX Staphylococcus aureus.
XX
XX US6180097-B1.
XX
XX 30-JAN-2001.
XX
XX 30-OCT-1998; 98US-00183437.
XX
XX 03-OCT-1989; 89US-00416530.
XX
XX 17-JAN-1990; 90US-00466577.
XX
XX 17-JAN-1991; 91WO-US000342.
XX
XX 01-JUN-1992; 92US-00891718.
XX
XX 02-MAR-1993; 93US-00025144.
XX
XX 31-JAN-1994; 94US-00189424.
XX
XX 19-JUN-1995; 95US-00491746.

XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 2001-158657/16.
 XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
 PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
 PT costimulatory molecule.
 XX Disclosure; Fig 2; 16pp; English.
 XX The present invention relates to a tumour cell capable of stimulating
 CC antitumor immune reactivity in vitro or in vivo contains and expresses an
 CC exogenous nucleic acid molecule encoding a superantigen or its active
 CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
 CC molecule that activates T cells in conjunction with an antigenic
 CC stimulus. The invention may be used for cancer therapy by stimulating an
 CC anticancer immune response in vivo or ex vivo
 XX Sequence 230 AA;
 XX
 XX Query Match 98.9%; Score 1224; DB 4; Length 230;
 XX Best Local Similarity 100.0%; Pred. No. 1.8e-114; Indels 0; Gaps 0;
 XX Matches 230; Conservative 0; Mismatches 0;
 QY 4 SEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHPW 63
 Db 1 SEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEK 123
 Db 61 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLTEK 120
 QY 124 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVORGL 183
 Db 121 KVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVORGL 180
 QY 184 IVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDKNKTINSENHLIDLXYTT 233
 Db 181 IVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDKNKTINSENHLIDLXYTT 230
 RESULT 6
 AAW35374 standard; peptide; 245 AA.
 XX AAW35374;
 XX 20-APR-1998 (first entry)
 XX Staphylococcus enterotoxin SEE wild-type superantigen.
 XX SEE; SEA; Staphylococcus enterotoxin; superantigen; conjugate; treatment;
 KW cancer; infection; autoimmune disease; antibody.
 XX Staphylococcus sp.
 XX Key Location/Qualifiers
 FT Misc-difference 20 /note= "can be mutated at this position"
 FT Misc-difference 21 /note= "can be mutated at this position"
 FT Misc-difference 24 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 FT Misc-difference 27 /note= "can be mutated at this position"
 XX WO9736932-A1.
 XX 09-OCT-1997.
 XX

PF 26-MAR-1997; 97WO-SE000537.
 XX 29-MAR-1996; 96SE-00001245.
 PR 12-AUG-1996; 96US-00695692.
 XX (PHAA) PHARMACIA & UPJOHN AB.
 XX Antonsson P, Hansson J, Bjoerk P, Dohlsten M, Kalland T;
 PI Abrahmeen L, Forsberg G;
 XX WPI; 1997-503052/46.
 XX Conjugate of target seeking moiety and modified superantigen - useful for
 PT activating the immune system to treat cancer, viral infections, parasitic
 PT infections and autoimmune diseases.
 XX Claim 4; Page 38-39; 58pp; English.
 XX This is the wild-type Staphylococcus enterotoxin SEE superantigen. This
 CC SEE superantigen can be modified to be used in a novel conjugate. The
 CC novel conjugate comprises a target seeking moiety and a modified wild
 CC type superantigen. The modified superantigen retains its ability to
 CC activate a subset of T cells, even though 1 or more wild-type amino acid
 CC residues in at least 1 region which functions in determining binding to T
 CC cell receptor (TCR) and activation of a subset of T cells has/have been
 CC replaced. Such a modified superantigen can optionally be used as part of
 CC a conjugate with a target seeking moiety, for activating the immune
 CC system to treat a mammalian disease. A pharmaceutical composition can be
 CC prepared comprising a modified antibody (preferably a Fab fragment fused
 CC to a peptide moiety providing activation of T cells in Vbeta specific
 CC manner) in which cysteines providing for interchain cysteine linkages in
 CC the native antibody have been replaced (preferably by serine residues) to
 CC prohibit cysteine formation. The modified wild-type superantigen is used
 CC for treating cancer, viral infections, parasitic infestations and
 CC autoimmune disease. The modified wild type superantigen has a lower
 CC immunogenicity and reactivity with neutralising antibodies and has fewer
 CC side-effects when used as a drug, compared to wild type superantigen
 XX Sequence 245 AA;
 XX
 XX Query Match 98.7%; Score 1222; DB 2; Length 245;
 XX Best Local Similarity 95.1%; Pred. No. 3.1e-114;
 XX Matches 233; Conservative 0; Mismatches 0; Indels 12; Gaps 1;
 QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 Db 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTCMYGGVTLHDNNRLT 120
 QY 121 ERKYPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 Db 121 ERKYPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDKNK-----TINSENHLIDL 228
 Db 181 RGLIVFHSSEGSTSVSYDLFDAQQYPTDLLRIYRDKNKTINSENHLIDLTYTINSENHLIDL 240
 QY 229 YLYTT 233
 Db 241 YLYTT 245
 RESULT 7
 ABP58457 standard; protein; 233 AA.
 XX ABP58457;
 XX AC ABP58457;
 XX DT 14-APR-2003 (first entry)
 XX

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
 DB 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
 QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNK-----TINSENLHIDL 228
 DB 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNK-----TINSENLHIDL 240
 QY 229 YLYTT 233
 DB 241 YLYTT 245

RESULT 9
 ABU79072
 ID ABU79072 standard; protein; 248 AA.
 XX ABU79072;
 AC ABU79072;
 XX 18-JUN-2003 (first entry)
 XX S. aureus SEE (staphylococcus enterotoxin E) protein.
 XX Superantigen; SAG; staphylococcal enterotoxin; tumour; cancer; apoptosis;
 KW Gene therapy; mammalian cell receptor; tumour associated lipid; energy;
 KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
 KW APC; antitumour.
 XX Staphylococcus aureus.
 OS
 XX US2002177551-A1.
 PN 28-NOV-2002.
 XX 30-MAY-2001; 2001US-00870759.
 PF 31-MAY-2000; 2000US-0208128P.
 PR (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 2003-361759/34.
 DR N-PSDB; ACA64698.
 XX A mammalian cell receptor, useful in the treatment of cancer by binding
 PT to tumor associated lipids where the binding induces energy or apoptosis
 PT in T cells and antigen presenting cells.
 XX Disclosure; Page; 167pp; English.

CC The invention relates to a mammalian cell receptor, useful in the
 CC treatment of cancer, which binds to tumour associated lipids and induces
 CC energy or apoptosis in the T cells and antigen presenting cells (APCs).
 CC Also included are a mammalian cell useful in the treatment of cancer
 CC where the receptor which binds tumour associated lipids and induces
 CC cellular inactivation or death is deleted or functionally deactivated,
 CC producing (M1) a tumouricidal immunocyte population in vivo in a mammal
 CC (by allowing tumour associated lipids to contact immunocytes in which
 CC receptors for immunosuppressive fatty acids, ceramides, glycolipids,
 CC sphingolipids, glycosphingolipids, phosphoglycolipids, gangliosides,
 CC sialylated glycans, lipopeptides and proteoglycolipids are inactivated or
 CC deleted), a construct useful in the treatment of cancer comprising a
 CC superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell

CC useful in the treatment of cancer (where an adaptor protein which
 CC inhibits T cell activation by tumour associated antigens is deleted or
 CC functionally deactivated), a composition useful in the treatment of
 CC cancer (comprising a lipid raft conjugated to a superantigen), producing
 CC (M2) a tumouricidal immunocyte population ex vivo in a mammal (by
 CC allowing tumour associated lipids to contact immunocytes, in which
 CC receptors for the lipids are inactivated or deleted to produce a
 CC tumouricidal immunocyte population, and administering the tumouricidal
 CC activated immunocytes to the host), producing (M3) a tumouricidal APC
 CC population ex vivo in a mammal (by allowing a tumour associated lipid to
 CC contact APCs, in which receptors for the tumour associated lipids are
 CC inactivated or deleted to produce a tumouricidal activated population,
 CC and administering APCs to the host), producing a tumouricidal T cell
 CC population ex vivo in a mammal) by allowing a tumour associated lipids to
 CC contact T cells, in which adaptor proteins, which inhibit T cell
 CC activation by tumour associated antigens, are deleted or functionally
 CC deactivated to produce a tumouricidal population of T cells, and
 CC administering the tumouricidal activated T cells to the host, or
 CC allowing a superantigen-lipid raft to contact T cells ex vivo, and
 CC administering the tumouricidal activated T cells to the host), treating
 CC (M5) cancer in a mammal (by administering a lipid binding molecule which
 CC binds immunosuppressive tumour associated lipids in vivo), producing (M6)
 CC a tumouricidal T cell population in vivo in a mammal (by allowing a
 CC tumour associated antigen to contact immunocytes in which adaptor
 CC proteins which inhibit T cell activation by tumour associated antigens
 CC are deleted or functionally deactivated) and producing (M7) a
 CC tumouricidal T cell population ex vivo in a mammal comprising allowing a
 CC superantigen-lipid raft conjugate to contact immunocytes in vivo. The
 CC receptors, methods and compositions are useful for treating cancers and
 CC tumours. Bacterial superantigens are co-administered or administered as
 CC fusion constructs with anti-tumour proteins or motifs. The present
 CC sequence represents a bacterial superantigen protein (e.g. a
 CC staphylococcal enterotoxin). Note: The sequence data for this patent did
 CC not form part of the printed specification, but was obtained in
 CC electronic format from the US patent office website at
 CC "seqdata.uspto.gov/sequence.html?docID=20020177551"
 XX

SQ Sequence 248 AA;
 Query Match 96.0%; Score 1188; DB 6; Length 248;
 Best Local Similarity 100.0%; Pred. No. 8.2e-111;
 Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGPFPTG 84
 QY 61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
 DB 85 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144
 QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
 DB 145 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 204
 QY 181 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNKNTINSENL 224
 DB 205 RGLIVFHSSEGSTSVSYDLFDAQGGYPTDLLRIYRDNKNTINSENL 248

RESULT 10
 ADF43296
 ID ADF43296 standard; protein; 248 AA.
 XX ADF43296;
 AC ADF43296;
 XX 12-FEB-2004 (first entry)
 DT Staphylococcal enterotoxin E polypeptide seq id 16.
 DE receptor; lipid-based tumour associated antigen; cytostatic;
 XX antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
 KW infectious disease; Staphylococcal enterotoxin E; SEE; enterotoxin E.

```

XX Staphylococcus.
XX OS
XX PN US2003157113-A1.
XX XX
XX PD 21-AUG-2003.
XX PF
XX PP 28-DEC-2000; 2000US-00751708.
XX XX
XX PR 28-DEC-1999; 99US-0173371P.
XX XX
XX PA (TERM/) TERMAN D S.
XX FI
XX PI Terman DS;
XX DR WPI; 2003-787326/74.
XX XX
XX PT New receptor in a mammalian cell that inhibits regular activation by
XX PT receptors specific for lipid-based tumor associated antigens, useful for
XX PT treating a neoplastic disease or tumor, and infectious diseases.
XX PS
XX PS Example 3; SEQ ID NO 16; 151pp; English.
XX CC
XX CC The invention describes a receptor in a mammalian cell that inhibits
XX CC regular activation by receptors specific for lipid-based tumor
XX CC associated antigen. The receptor has cytostatic and antimicrobial
XX CC properties and is suitable for use in gene therapy. The receptors,
XX CC methods and compositions are useful for treating a neoplastic disease or
XX CC tumour (cancer), and infectious diseases. This is the amino acid sequence
XX CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
XX CC transfected in to a cell alone or with DNA encoding a cell surface moiety
XX CC to generate antitumour immunity.
XX SQ
XX SQ Sequence 248 AA;
XX
XX Query Match 96.0%; Score 1188; DB 7; Length 248;
XX Best Local Similarity 100.0%; Pred. No. 8.2e-111;
XX Matches 224; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
Qy 1 SEKEEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLPKGPTG 60
Db 25 SEKEEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLPKGPTG 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLT 144
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 224
Db 205 RGLIVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSEN 248
XX
XX RESULT 11
XX AAR45012
XX ID AAR45012 standard; protein; 230 AA.
XX AC
XX AC AAR45012;
XX XX
XX DT 25-MAR-2003 (revised)
XX DT 08-JUN-1994 (first entry)
XX XX
XX DE Staphylococcal enterotoxin SEE.
XX KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
XX KW autoimmune disease; toxicity; Protein A; perfusion system.
XX OS
XX OS Staphylococcus aureus.
XX PH Key Location/Qualifiers

```

```

FT Misc-difference 120
FT /note= "Given in the specification as J, no further
FT details given"
FT Misc-difference 121
FT /note= "Given in the specification as J, no further
FT details given"
FT Misc-difference 123
FT /note= "Given in the specification as O, no further
FT details given"
FT Misc-difference 124
FT /note= "Given in the specification as U, no further
FT details given"
XX
XX WO9324136-A1.
XX
XX PD 09-DEC-1993.
XX
XX PF 01-JUN-1993; 93WO-US005213.
XX
XX PR 01-JUN-1992; 92US-00891718.
XX
XX (TERM/) TERMAN D S.
XX (STON/) STONE J L.
XX
XX Terman DS, Stone JL;
XX
XX WPI; 1993-405418/50.
XX
XX Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
XX PT in a patient or for the treatment of auto-immune diseases.
XX PS
XX PS Disclosure; Fig 1; 90pp; English.
XX
XX CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
XX CC which may be used in the methods of the invention for treating cancer in
XX CC a patient. These SEs, and homologues of them, can be used as tumouricidal
XX CC agents for treating cancers and autoimmune disease. They exhibit
XX CC tumouricidal activity and toxicity identical to that observed for the
XX CC Protein A perfusion system. They may be administered by i.v. injection.
XX CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX SQ Sequence 230 AA;
XX
XX Query Match 95.2%; Score 1179; DB 2; Length 230;
XX Best Local Similarity 96.1%; Pred. No. 6e-110;
XX Matches 221; Conservative 3; Mismatches 6; Indels 0; Gaps 0;
XX
Qy 4 SEEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLPKGPTGHPW 63
Db 1 SEEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLPKGPTGHPW 60
Qy 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123
Db 61 YNDLLVDKSGKDATNKYKGVLDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
Qy 124 KVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 183
Db 121 VXXYBKWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Qy 184 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENLIHDIYLYTT 233
Db 181 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENMHIDIYLYTT 230
XX
XX RESULT 12
XX ABB76235
XX ID ABB76235 standard; protein; 230 AA.
XX AC
XX AC ABB76235;
XX XX
XX DT 09-AUG-2002 (first entry)
XX DE Staphylococcus aureus enterotoxin E.

```

XX Enterotoxin E; SEE, superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 XX Staphylococcus aureus.
 OS
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 120 /note= "given as 'J' in the specification"
 FT Misc-difference 121 /note= "given as 'J' in the specification"
 FT Misc-difference 123 /note= "given as 'O' in the specification"
 FT Misc-difference 124 /note= "given as 'U' in the specification"
 FT Misc-difference 125 /note= "given as 'V' in the specification"
 FT
 XX US2002051765-A1.
 PN XX
 PD XX
 XX 02-MAY-2002.
 XX 19-DEC-2000; 2000US-00741503.
 XX 03-OCT-1989; 89US-00416530.
 PR 17-JAN-1990; 90US-00466577.
 PR 17-JAN-1991; 91WO-US000342.
 PR 01-JUN-1992; 92US-00891718.
 PR 02-MAR-1993; 93US-00025144.
 PR 31-JAN-1994; 94US-00189424.
 PR 19-JUN-1995; 95US-00491746.
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 2002-415198/44.
 DR
 XX Reagent for treating cancer without the need for e.g. radiotherapy,
 PT comprises a specific V beta subset of T cells sensitized to a growing
 PT tumor and stimulated with superantigens.
 XX Disclosure; Fig 2; 17pp; English.
 PS
 XX The present sequence is the protein sequence of enterotoxin E (SEE) of
 CC Staphylococcus aureus. Similarity is shown, in several stretches of
 CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
 CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
 CC present invention, synthetic polypeptides useful in tumour therapy and in
 CC blocking or destroying autoreactive T and B lymphocyte populations are
 CC characterised by substantial structural homology to staphylococcal
 CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
 CC exotoxins, with statistically significant sequence homology and
 CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
 CC analysis exceeding 6) to include alignment of cysteine residues and
 CC similar hydropathy profiles. These superantigens are used to treat solid
 CC tumours, including their metastases, without radiation, surgery or
 CC standard chemotherapeutic agents. A claimed method of human cancer
 CC treatment involves contacting haematopoietic cells from a patient with
 CC one or more superantigens ex vivo to generate stimulated cells, selecting
 CC a specific V beta subset of cells, and reintroducing these cells into the
 CC patient to induce an in vivo therapeutic, tumouricidal reaction
 XX
 SQ Sequence 230 AA;
 Query Match 94.9%; Score 1175; DB 5; Length 230;
 Best Local Similarity 96.1%; Pred. No. 1.5e-109;
 Matches 221; Conservative 2; Mismatches 7; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDQFLENTLLFKGFFTGHPW 60

QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123
 DB YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 183
 DB YVXXKXWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 180
 QY 184 IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENHLIDLYLYTT 233
 DB IVFHSSEGSTVSVDLFDAGQGYPTDLLRIYRDNKTINSENWHIDYLYTT 230
 RESULT 13
 AARI13204
 ID AARI13204 standard; protein; 230 AA.
 XX
 AC AARI13204;
 XX 15-OCT-1991 (first entry)
 DT
 XX Staphylococcal enterotoxin E.
 DE
 XX SEE; cancer treatment; pyrogen; tumouricide.
 KW
 XX Staphylococcus aureus.
 OS
 PN WO9110680-A.
 XX 25-JUL-1991.
 PD
 XX 17-JAN-1990; 90US-00466577.
 PF
 XX 17-JAN-1990; 90US-00466577.
 PR
 XX (TERM/) TERMAN D S.
 PA Terman DS;
 XX WPI; 1991-237984/32.
 DR
 XX Treating cancer with enterotoxin from Staphylococcus aureus -
 PT administered by IV injection, having same tumoricidal activity as
 PT Staphylococcal protein A without potential toxic reactions.
 XX Disclosure; Fig 1; 74pp; English.
 PS
 XX SEE was isolated and purified from S.aureus. It can be used for treating
 CC cancer, activating cytokine mediators and procoagulant systems,
 CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
 CC administered intravenously, optionally with ibuprofen to attenuate toxic
 CC reaction to SEE. Synthetic polypeptides having structural homology to
 CC Staphylococcal exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydropathy profiles. See AARI13203-R13211
 XX Sequence 230 AA;
 Query Match 93.4%; Score 1156; DB 2; Length 230;
 Best Local Similarity 93.9%; Pred. No. 1.2e-107;
 Matches 216; Conservative 6; Mismatches 8; Indels 0; Gaps 0;
 QY 4 SEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDQFLENTLLFKGFFTGHPW 63
 DB 1 SEINEKDLRKSELOALNSLNRQIYYNKAITENKESDDQFLENTLLFKGFFTGHPW 60
 QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEK 123
 DB YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGTGNKTACMYGGVTLHDNNRLTEEX 120
 QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 183
 DB YVXXKXWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQVGL 180

Qy	184	IVFHSSEGSTVSYDLFDAGQGYPTDLLRIYRDNKTINSENHLHIDLYLVT	233
Db	181	IVFHSSEGSTVSYDLFDAGQGYPTDLLRIYRDNKTINSENHMDIYLVTT	230
RESULT 14			
ABP58455			
ID	ABP58455	standard; protein; 233 AA.	
XX			
AC	ABP58455;		
XX			
DT	14-APR-2003	(first entry)	
XX			
XX	Engineered superantigen SEA/E-120	for human cancer therapy.	
XX			
XX	Superantigen; staphylococcal enterotoxin; antibody; cancer; tumour;		
KW	cytotoxic; vaccine; SEA/E-120; mutant; mutein.		
XX			
OS	Staphylococcus sp.		
OS	Synthetic.		
XX			
PH	Key	Location/Qualifiers	
FT	Misc-difference 20	/note= "wild-type Arg substituted by Gly"	
FT	Misc-difference 21	/note= "wild-type Asn substituted by Thr"	
FT	Misc-difference 24	/note= "wild-type Ser substituted by Gly"	
FT	Misc-difference 27	/note= "wild-type Arg substituted by Lys"	
FT	Misc-difference 79	/note= "wild-type Lys substituted by Glu"	
FT	Misc-difference 81	/note= "wild-type Lys substituted by Glu"	
FT	Misc-difference 83	/note= "wild-type Lys substituted by Ser"	
FT	Misc-difference 84	/note= "wild-type Lys substituted by Ser"	
FT	Misc-difference 227	/note= "wild-type Asp substituted by Ser"	
XX			
PN	WO2003002143-A1.		
XX			
PD	09-JAN-2003.		
XX			
PF	19-JUN-2002; 2002WO-SE001188.		
XX			
PR	28-JUN-2001; 2001SE-00002327.		
XX			
PA	(ACTI-) ACTIVE BIOTECH AB.		
XX			
PI	Forsberg G, Erlandsson E, Antonsson P, Walse B;		
DR	WPI; 2003-201467/19.		
XX			
PT	Conjugate for therapy, has bacterial superantigen with a region in T-cell		
PT	receptor and four regions to determine binding to class II major		
PT	histocompatibility complex, antibody to cancer associated cell surface		
PT	structure.		
XX			
PS	Claim 8; Fig 2; 102pp; English.		
XX			
CC	The present sequence is the protein sequence of engineered staphylococcal		
CC	superantigen SEA/E-120. The superantigen is derived from staphylococcal		
CC	enterotoxin E (SEE) by the incorporation of the following amino acid		
CC	substitutions to reduce seroreactivity whilst maintaining production		
CC	levels and biological activity: R20G, N21T, S24G, R27K, K79E, K81E, K83S		
CC	and D227S. SEA/E-120 has been genetically fused to the Fab moiety of the		
CC	tumour reactive antibody 5T4 to form a claimed conjugate (see ABP58454)		
CC	designed to target and destroy cancer cells, including cancer of the		
CC	lung, breast, colon, kidney, pancreas, ovary, stomach, cervix and		
CC	prostate (claimed)		

FT	Misc-difference 452	/note= "wild-type Asp substituted by Ser"	
FT	Region 459. .565	/note= "5T4 variable light chain"	
FT	Misc-difference 469	/note= "wild-type Phe substituted by Ser"	
FT	Misc-difference 504	/note= "wild-type Thr substituted by Lys"	
FT	Misc-difference 522	/note= "wild-type Ile substituted by Ser"	
FT	Misc-difference 532	/note= "wild-type Phe substituted by Leu"	
FT	Misc-difference 536	/note= "wild-type Thr substituted by Ser"	
FT	Misc-difference 537	/note= "wild-type Leu substituted by Val"	
FT	Misc-difference 542	/note= "wild-type Leu substituted by Ala"	
FT	Region 566. .672	/note= "C242 constant light chain"	
XX	WO2003002143-A1.		
PN	09-JAN-2003.		
XX	19-JUN-2002; 2002WO-SE001188.		
XX	28-JUN-2001; 2001SE-00002327.		
XX	(ACTI-) ACTIVE BIOTECH AB.		
XX	Forsberg G, Erlandsson E, Antonsson P, Walse B;		
PI	WPI; 2003-201467/19.		
DR	Conjugate for therapy, has bacterial superantigen with a region in T-cell		
XX	receptor and four regions to determine binding to class II major		
PT	histocompatibility complex, antibody to cancer associated cell surface		
PT	structure.		
XX	Claim 12; Fig 10; 102pp; English.		
XX	The present sequence is a conjugate of a bacterial superantigen and an		
CC	antibody moiety, and has been designed to target and destroy cancer		
CC	cells. The bacterial superantigen is SEA/E-120 (see also ABP58455), which		
CC	was derived from staphylococcal enterotoxin B (SEB) by the incorporation		
CC	of the following amino acid substitutions to reduce seroreactivity whilst		
CC	maintaining production levels and biological activity: K20G, N21T, S24G,		
CC	R27K, K79E, K81S, K83S and D227S. SEA/E-120 was genetically fused to the		
CC	Fab moiety of the tumour reactive antibody 574. Substitutions were made		
CC	in the 574 sequence to obtain higher yields: in the heavy chain, H41P,		
CC	S44G, I69T and V113G; and in the light chain, F10S, T45K, I63S, F73L,		
CC	T77S, L78V and L83A. An expression vector comprising DNA encoding the		
CC	conjugate can be used to transform host cells for recombinant production		
CC	of the conjugate. The conjugate is useful for treating cancer, including		
CC	cancer of the lung, breast, colon, kidney, pancreas, ovary, stomach,		
CC	cervix and prostate (claimed)		
XX	Sequence 672 AA;		
SQ	Query Match 89.4%; Score 1107; DB 6; Length 672;		
	Best Local Similarity 89.7%; Pred. No. 4.9e-102;		
	Matches 209; Conservative 9; Mismatches 15; Indels 0; Gaps 0;		
QY	1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60		
DB	226 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 285		
QY	61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120		
DB	286 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 345		
QY	121 EKKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGKVKQ 180		

Db	346 EKKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGKVKQ 405		
QY	181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233		
Db	406 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 458		
RESULT 16			
AAR13203			
ID	AAR13203 standard; protein; 233 AA.		
XX	AC AAR13203;		
XX	DT 15-OCT-1991 (first entry)		
XX	DE Staphylococcal enterotoxin A.		
XX	KW SEA; cancer treatment; pyrogen; tumouricide.		
XX	OS Staphylococcus aureus.		
XX	PN WO9110680-A.		
XX	PD 25-JUL-1991.		
XX	PF 17-JAN-1990; 90US-00466577.		
XX	PR 17-JAN-1990; 90US-00466577.		
XX	PA (TERM/) TERMAN D S.		
XX	PI Terman DS;		
XX	WPI; 1991-237984/32.		
XX	Treating cancer with enterotoxin from Staphylococcus aureus -		
PT	administered by IV injection, having same tumoricidal activity as		
PT	Staphylococcal protein A without potential toxic reactions.		
XX	Disclosure; Fig 1; 74pp; English.		
XX	SEA was isolated and purified from S.aureus. It can be used for treating		
CC	cancer, activating cytokine mediators and procoagulant systems,		
CC	augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be		
CC	administered intravenously, optionally with ibuprofen to attenuate toxic		
CC	reaction to SEA. Synthetic polypeptides having structural homology to		
CC	Staphylococcal exotoxins are claimed, provided the homology includes		
CC	statistically significant sequence homology, alignment of Cysteine		
CC	residues and similar hydropathy profiles. See also AAR13204-R13211		
XX	Sequence 233 AA;		
SQ	Query Match 83.6%; Score 1035; DB 2; Length 233;		
	Best Local Similarity 82.8%; Pred. No. 1.9e-95;		
	Matches 193; Conservative 17; Mismatches 23; Indels 0; Gaps 0;		
QY	1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60		
DB	1 SEKSEINEKDLRKXSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60		
QY	61 HPWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120		
DB	61 HSWYNLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACWGGVTLHDNNRLT 120		
QY	121 EKKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGKVKQ 180		
DB	121 EKKKVPINLWIDGKQTTVPIDKVKTSKKEVTQVELDLQARHYLHGKFGLYNSDSFGKVKQ 180		
QY	181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233		
DB	181 RGLIVFHSSEGSTVSVDLFDAGQYPTDLLRIYRDNKTINSENHLIDLYLTT 233		

RESULT 17
ABP58458
ID ABP58458 standard; protein; 233 AA.
XX AC
XX ABP58458;
XX AC
XX 14-APR-2003 (first entry)
XX DT
XX DE Staphylococcal enterotoxin A.
XX DE Superantigen; staphylococcal enterotoxin A; antibody; cancer; tumour;
XX KW cytostatic; vaccine.
XX KW
XX OS Staphylococcus sp.
XX OS
XX PN WO2003002143-A1.
XX PD
XX PF 09-JAN-2003.
XX PF 19-JUN-2002; 2002WO-SE001188.
XX PR 28-JUN-2001; 2001SE-00002327.
XX PA (ACTI-) ACTIVE BIOTECH AB.
XX PI Forsberg G, Erlandsson E, Antonsson P, Walse B;
XX PI WPI; 2003-201467/19.
XX DR
XX CC Conjugate for therapy, has bacterial superantigen with a region in T-cell
XX PT receptor and four regions to determine binding to class II major
XX PT histocompatibility complex, antibody to cancer associated cell surface
XX PT structure.
XX PS
XX FS Example 3; Fig 3; 102pp; English.
XX CC The present sequence is the protein sequence of staphylococcal
XX CC enterotoxin A (SEA). The invention provides novel conjugates (see
XX CC ABP58454) for human cancer therapy. These comprise an engineered
XX CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
XX CC antibody moiety, such as tumour reactive antibody 5T4. Bacterial
XX CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
XX CC modelling of the engineered superantigens. The superantigens were
XX CC engineered to reduce seroreactivity whilst maintaining biological
XX CC activity and production levels. The novel conjugates were designed to
XX CC target and destroy cancer cells, including cancer of the lung, breast,
XX CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
XX CC
SQ Sequence 233 AA;
Query Match 82.6%; Score 1023; DB 6; Length 233;
Best Local Similarity 82.0%; Pred. No. 3e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60
Db 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 61 HSWYNDLLVDFDSKDI VDKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVG 180
Db 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVG 180
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLIYRDNKTINSENHLDIYLTT 233
Db 181 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKTINSENHLDIYLTS 233

AAU14104
ID AAU14104 standard; peptide; 257 AA.
XX AC
XX AAU14104;
XX DT
XX DT 21-NOV-2001 (first entry)
XX XX
XX DE Peptide sequence from Staphylococcus aureus enterotoxin A.
XX DE Anti-retroviral; DPl78-like; DPl07-like; enterotoxin A; antifusogenic;
XX KW antiviral; HIV transmission.
XX OS Staphylococcus aureus.
XX OS
XX PN WO200151673-A2.
XX XX
XX PD 19-JUL-2001.
XX PF 05-JUL-2000; 2000WO-US035727.
XX PF 09-JUL-1999; 99US-00350841.
XX PR (TRIM-) TRIMERIS INC.
XX PA
XX PI Jeffs P, Lackey JW, Erickson JB, Lawless MK, Merutka G;
XX PI WPI; 2001-442157/47.
XX DR
XX XX
XX PT Identifying a compound that inhibits the formation of or disrupts a
XX PT DPl07/DPl78 complex, especially compounds with antifusogenic, antiviral
XX PT or intracellular modulatory activity, by detecting the formation of a
XX PT DPl07/DPl78 complex.
XX XX
XX PS Disclosure; Fig 42; 259pp; English.
XX CC
XX CC The present invention relates to peptides which exhibit anti-retroviral
XX CC activity. The peptides of the invention (AAU12559-AAU14009) comprise
XX CC DPl78-like and DPl07-like peptides. The DPl78 peptide corresponds to
XX CC amino acids 639-673 of the transmembrane protein gp41 from human
XX CC immunodeficiency virus 1 (HIV-1) isolate LAI. The DPl07 peptide
XX CC corresponds to amino acids 558-595 of gp41 from HIV-1LAI. The invention
XX CC also relates to a method of identifying compounds that inhibit the
XX CC formation of or disrupts a DPl07/DPl78 complex. The method comprises
XX CC detecting the formation of a DPl07/DPl78 complex, both in the presence or
XX CC absence of a test compound, in a reaction mixture containing DPl07 and
XX CC DPl78 peptides. The method is useful for identifying compounds, including
XX CC small molecule compounds, which may themselves exhibit antifusogenic,
XX CC antiviral or intracellular modulatory activity. The DPl78-like/DPl07-like
XX CC peptides are useful to inhibit human and non-human retroviral,
XX CC particularly HIV, transmission to uninfected cells. The present sequence
XX CC represents a peptide sequence from Staphylococcus aureus enterotoxin A
XX CC
SQ Sequence 257 AA;
Query Match 82.6%; Score 1023; DB 4; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGPF TG 60
Db 25 SEKSEINEKDLRKSELRNALSRLQIYYNEKAITENKESDDQFLENTLLFKGPF TG 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDFDSKDI VDKYKGVVDLYGAYGYQCAGGTENKACMYGGVTLHDNNRLT 144
Qy 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVG 180
Db 145 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYNSDSFGKVG 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLIYRDNKTINSENHLDIYLTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKTINSENHLDIYLTS 257


```

RESULT 19
ABO10269
ID ABO10269 standard; protein; 257 AA.
XX
XX ABO10269;
XX
XX 19-AUG-2003 (first entry)
XX
XX S. aureus enterotoxin A.
XX
XX HIV; DP107; DP178; glycoprotein 41; antiviral; virucide; EBV;
XX Epstein-Barr virus infection; heptad repeat motif.
XX
XX Staphylococcus aureus.
XX
XX US6518013-B1.
XX
XX 11-FEB-2003.
XX
XX 07-JUN-1995; 95US-00485546.
XX
XX 07-JUN-1993; 93US-00073028.
XX
XX 07-JUN-1994; 94US-00255208.
XX
XX 20-DEC-1994; 94US-00360107.
XX
XX (TRIM-) TRIMERIS INC.
XX
XX Barney SO, Lambert DM, Petteway SR;
XX
XX WPI; 2003-465599/44.
XX
XX Inhibiting transmission of Epstein-Barr virus to a cell, by contacting
XX the cell with a peptide consisting of a region of Epstein-Barr virus
XX protein.
XX
XX Example; Fig 42; 716pp; English.
XX
XX The invention relates to inhibiting (M) transmission of an Epstein-Barr
XX virus to a cell, comprising contacting the cell with an effective
XX concentration of a peptide consisting of a region of 16-39 consecutive
XX amino acids of an Epstein-Barr virus protein for an effective period of
XX time, where the region is recognised by one or more of ALLMOTIF5,
XX 107x178x4 or PLZIP sequence search motifs, the peptide further comprises
XX an amino terminal X, and a carboxy terminal Z in which X comprises an
XX amino group, acetyl group, 9-fluorenylmethoxy-carbonyl group, hydrophobic
XX group or macromolecular carrier group, and Z comprises a carboxyl group,
XX amide group, hydrophobic group, or macromolecular carrier group, and
XX fusion of the virus to the cell is inhibited. The peptides were
XX identified by analysing the structure/motifs present in the HIV-1
XX glycoprotein 41 anti-HIV peptides DP107 and DP178. These heptad repeat
XX motif containing peptides were used to design the motifs cited above,
XX which in turn were used to analyse proteins from other pathogenic
XX organisms and HIV isolates, looking for DP107/178 structural analogues.
XX The method is useful for inhibiting transmission of Epstein-Barr virus to
XX a cell and Epstein-Barr virus infection. The present sequence is a
XX protein from a pathogenic organism analysed for regions analogous to
XX DP107 or DP178
XX
XX Sequence 257 AA;

Query Match 82.6%; Score 1023; DB 6; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

RESULT 20
ADD44368
ID ADD44368 standard; protein; 257 AA.
XX
XX ADD44368;
XX
XX 15-JAN-2004 (first entry)
XX
XX Staphylococcus aureus enterotoxin A protein.
XX
XX enterotoxin A; ent A; food poisoning; bacterium; food; milk; fruit juice;
XX ice cream.
XX
XX Staphylococcus aureus.
XX
XX WO2003080865-A1.
XX
XX 02-OCT-2003.
XX
XX 26-MAR-2002; 2002WO-IB001150.
XX
XX 26-MAR-2002; 2002WO-IB001150.
XX
XX (COUL ) COUNCIL SCI & IND RES.
XX
XX Padmapriya BP, Ramesh A, Chandrashekar A, Varadaraj MC;
XX
XX WPI; 2003-779273/73.
XX
XX N-PSDB; ADD44369.
XX
XX Novel oligonucleotide primers directed against enterotoxin A gene of
XX Staphylococcus aureus and heat stable enterotoxin gene of Yersinia
XX enterocolitica, useful for detecting food poisoning causing bacteria.
XX
XX Example 2; Page 14-15; 34pp; English.
XX
XX The invention relates to novel oligonucleotide primers directed against
XX enterotoxin A gene (ent A) of Staphylococcus aureus and heat stable
XX enterotoxin gene (yst) of Yersinia enterocolitica. The novel
XX oligonucleotide primers are useful for simultaneously detecting food
XX poisoning bacterial species Staphylococcus aureus and/or Yersinia
XX enterocolitica in food systems e.g., milk, fruit juices and ice creams,
XX without prior enrichment for preventing food poisoning outbreak. The PCR
XX detection method is useful for detecting the bacteria strains in quantity
XX as low as one cell. The method can be directly used for detecting
XX bacterial strains. The oligonucleotide primers allow quick and highly
XX sensitive detection of the food poisoning bacterial species. This
XX sequence represents the protein derived from the enterotoxin A gene from
XX Staphylococcus aureus of the invention.
XX
XX Sequence 257 AA;

Query Match 82.6%; Score 1023; DB 7; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFFTG 84

QY 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNLLVDLGSKDIIVDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 144

```

```
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 BEKKVPINLWIDGKQNTVPLETVTKNKQNTVQELDLQARHYLQEKYLNYSNDSVDFGKVQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLIDLYLTT 233
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 21
ADH10956
ID ADH10956 standard; protein; 257 AA.
XX
AC ADH10956;
XX
DT 11-MAR-2004 (first entry)
DE Enterotoxin A protein.
KW Enterotoxin A; Computational design; protein binding peptide;
KW hydrophobic potential; solvent contact surface;
KW protein three-dimensional structure; two-dimensional characteristic map;
KW Fourier transformation.
XX
OS Staphylococcus aureus.
XX
PN JP2003263465-A.
XX
PD 19-SEP-2003.
XX
PF 07-MAR-2002; 2002JP-00062348.
XX
PR 07-MAR-2002; 2002JP-00062348.
XX
PA (ENKA-) ENKAKU IRYO KENKYUSHO KK.
XX
DR WPI; 2004-075279/08.
XX
PT Designing and selecting protein binding peptide by identifying peptide
PT binding region of protein, and designing peptides that bind to the region
PT using structure-biological activity relationship program of computer.
XX
PS Example; SEQ ID NO 1, 11pp; Japanese.
XX
CC The invention relates to a method for computational design and selection
CC of protein binding peptides, comprising computing the hydrophobic
CC potential of all surface points arranged on the solvent contact surface
CC of a protein three-dimensional structure, developing a two-dimensional
CC characteristic map by a self-assembly method, identifying a region of
CC hydrophobic amino acids by Fourier transformation and designing a protein
CC binding peptide corresponding to the hydrophobic region. The method is
CC useful for designing and selecting protein binding peptides. This
CC sequence represents an Enterotoxin A protein used in the scope of the
CC invention.
XX
SQ Sequence 257 AA;

Query Match 82.6%; Score 1023; DB 8; Length 257;
Best Local Similarity 82.0%; Pred. No. 3.5e-94;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKXSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTG 60
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 25 SEKSEINEKDLRKXSELQGTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFTD 84

QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGQACGTPNKTCMYGGVTLHDNNRLT 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 HSWYNDLLVDFDSKDIVDKYKGGKVDLYGAYYGQACGTPNKTCMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 BEKKVPINLWIDGKQNTVPLETVTKNKQNTVQELDLQARHYLQEKYLNYSNDSVDFGKVQ 204
```

```
QY 181 RGLIVFHSSEGSTVSYDLFDAQGOYPTLLRIYRDNKTINSENHLIDLYLTT 233
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 205 RGLIVFHTSTEPSVNYDLFGAQGOYSNTLLRIYRDNKTINSENHMDIYLYTS 257

RESULT 22
AAW06738
ID AAW06738 standard; protein; 233 AA.
XX
AC AAW06738;
XX
DT 08-MAR-1997 (first entry)
DE Staphylococcus enterotoxin A.
KW Enterotoxin A; superantigen; antigen; cytokine; chemokine; T cell;
KW lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW adjuvant.
XX
OS Staphylococcus sp.
XX
PN WO9636366-A1.
XX
PD 21-NOV-1996.
XX
PF 20-MAY-1996; 96WO-US007432.
XX
PR 18-MAY-1995; 95US-00446918.
XX
PR 29-DEC-1995; 95US-00580806.
XX
PA (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI Dow SW, Elmslie RE, Potter TA;
XX
DR WPI; 1997-011857/01.
XX
DR N-PSDB; AAT45699.
XX
PT Recombinant molecule encoding superantigen and opt. cytokine or
PT chemokine controls activity of effector cells (T cells, monocytes,
PT natural killer cells), used for gene therapy of cancer.
XX
PS Example 1; Page 98-99; 131pp; English.
XX
CC A cDNA clone (AAT45699) codes for staphylococcal enterotoxin A (AAW06738)
CC superantigen. Nucleic acids encoding superantigens (see also AAW06737,
CC AAW06739), esp. truncated forms of the superantigen lacking the leader
CC peptide, can be used in the gene therapy of cancer, infectious diseases
CC and immunological disorders. The nucleic acid, optionally in combination
CC with cytokine or chemokine nucleic acids, is delivered to an animal using
CC e.g. liposomes. It acts by controlling the activity of effector cells,
CC such as T-cells, macrophages, monocytes and/or natural killer cells.
CC Localised prodn. of an effective but non-toxic amount of encoded proteins
CC allows safe treatment of the animal
XX
SQ Sequence 233 AA;

Query Match 82.3%; Score 1019; DB 2; Length 233;
Best Local Similarity 81.9%; Pred. No. 7.7e-94;
Matches 190; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKXSELQNALSNLROIYYNEKAITENKESDDOFLNTLLFKGFTGH 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 2 EKSEINEKDLRKXSELQGTALGNLKOIYYNEKAKTENKESHQFLQHTILFKGFTDH 61

QY 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYYGQACGTPNKTCMYGGVTLHDNNRLTE 121
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 62 SWYNDLLVDFDSKDIVDKYKGGKVDLYGAYYGQACGTPNKTCMYGGVTLHDNNRLTE 121

QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 181
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 122 EKKVPINLWIDGKQNTVPLETVTKNKQNTVQELDLQARHYLQEKYLNYSNDSVDFGKVQ 181
```



```

Db      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120
      121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Qy      121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db      121 EEKVPINLWDGKQTTVPLETVTNKKNVTVQELDLQARRYLQEKYLYNSDVFDDGKVQ 180
Qy      181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHIDLTYTT 233
      181 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRLRIYRDNKTINSENMMHIDIYLYTS 233
Db      181 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRLRIYRDNKTINSENMMHIDIYLYTS 233

RESULT 25
AAB67338
ID AAB67338 standard; peptide; 233 AA.
XX
AC AAB67338;
XX
DT 23-APR-2001 (first entry)
XX
DE Staphylococcus aureus enterotoxin A protein.
XX
KW Tumour; cancer; immune; enterotoxin.
XX
OS Staphylococcus aureus.
XX
PN US6180097-B1.
XX
PD 30-JAN-2001.
XX
PF 30-OCT-1998; 98US-00183437.
XX
PR 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-0000342.
PR 01-JUN-1992; 92US-00891718.
PR 02-MAR-1993; 93US-00025144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX
FA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
DR WPI; 2001-158657/16.
XX
PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
PT costimulatory molecule.
XX
PS Disclosure; Fig 2; 16pp; English.
XX
CC The present invention relates to a tumour cell capable of stimulating
CC antitumor immune reactivity in vitro or in vivo contains and expresses an
CC exogenous nucleic acid molecule encoding a superantigen or its active
CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
CC molecule that activates T cells in conjunction with an antigenic
CC stimulus. The invention may be used for cancer therapy by stimulating an
CC anticancer immune response in vivo or ex vivo
XX
SQ Sequence 233 AA;
      Query Match      82.1%; Score 1016; DB 4; Length 233;
      Best Local Similarity 81.5%; Pred. No. 1.5e-93;
      Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

Qy      1 SEKSEINEKDLRKKSELQNALSNLRQIYYNKEAITEKESDDQFLNTLLFKGFPTG 60
      1 SEKSEINEKDLRKKSELQGTALGNLQIYYNKEAKTENKESHQDQLHTILFKGFPTD 60
Db      61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120
Qy      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120
Db      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120

```

```

Qy      121 EEKVPINLWDGKQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
      121 EEKVPINLWDGKQTTVPLETVTNKKNVTVQELDLQARRYLQEKYLYNSDVFDDGKVQ 180
Qy      181 RGLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSENHLHIDLTYTT 233
      181 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRLRIYRDNKTINSENMMHIDIYLYTS 233
Db      181 RGLIVFHTSTEPSVNYDLFGAGQGYSNLTLRLRIYRDNKTINSENMMHIDIYLYTS 233

RESULT 26
AAR45011
ID AAR45011 standard; protein; 233 AA.
XX
AC AAR45011;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcus aureus enterotoxin SEA.
XX
KW Staphylococcus aureus enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
PN WO9324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
FA (TERM/) TERMAN D S.
XX
PI (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
DR WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumouricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumouricidal activity and toxicity identical to that observed for the
CC protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 233 AA;
      Query Match      81.8%; Score 1013; DB 2; Length 233;
      Best Local Similarity 81.5%; Pred. No. 3.1e-93;
      Matches 190; Conservative 16; Mismatches 27; Indels 0; Gaps 0;

Qy      1 SEKSEINEKDLRKKSELQNALSNLRQIYYNKEAITEKESDDQFLNTLLFKGFPTG 60
      1 SEKSEINEKDLRKKSELQGTALGNLQIYYNKEAKTENKESHQDQLHTILFKGFPTD 60
Db      61 HPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120
Qy      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120
Db      61 HSWYNDLLVDFDSKDIDVKYKGGKVDLYGAYYGQACGTENKTACMYGGVTLHDNNRLT 120

```


Qy 181 RGLIVFHSSEGSTVSYDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGVSNLTLLRIYRDNKTINSENHIDILYLYTS 257

RESULT 32
ID ABU62324 standard; protein; 257 AA.
XX AC ABU62324;
XX DT 27-AUG-2003 (first entry)
XX DE S. aureus periplasmic enterotoxin A mutant #1.
KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX OS Staphylococcus aureus.
OS Synthetic.

XX FH Key Location/Qualifiers
FT Peptide 1..24
FT Protein /label= Signal_peptide
FT /label= Mature_SEA_mutant #1
FT Misc-difference 66 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 72 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 94 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 113 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 116 /note= "Wild-type Tyr substituted by Ala"
XX US2003036644-A1.
XX PD 20-FEB-2003.
XX PF 26-NOV-2001; 2001US-00002784.
XX PR 25-JUN-1997; 97US-00882431.
XX PR 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX PI ULRICH RG;
XX WPI; 2003-492125/46.
XX DR N-PSDB; ACD28894.
XX New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
XX Disclosure; Page 22-23; 68pp; English.

XX The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), CC treating/ameliorating a superantigen-associated bacterial infection, an CC antiserum isolated from individuals immunised with one or more altered CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-

CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, CC SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and CC SPEb). The superantigen toxin DNA fragment is useful for preparing a CC composition for treating or preventing bacterial infection. The present CC sequence represents the L42E/L48R/D70R/Y89G/Y92A (with reference to the CC mature protein sequence) mutant of periplasmic SEA
XX SQ Sequence 257 AA;
Query Match 80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 7.2e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
Qy 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 25 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTG 84
Qy 61 HPWYNDLLVLDGSKDATNKYKGVLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKDI VDKYKGVLYGAYGYOCAGGTPNKTCMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGKQNTVPLETVTNKKNVTVOELDLQARHYLHGKGLYNSDSFGGKVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLFDAGQGVPTLLRIYRDNKTINSENHIDILYLYTT 233
Db 205 RGLIVFHTSTEPSVNYDLFGAQGVSNLTLLRIYRDNKTINSENHIDILYLYTS 257

RESULT 33
AAE37676
ID AAE37676 standard; protein; 257 AA.
XX AC AAE37676;
XX DT 06-OCT-2003 (first entry)
XX DE Protein #1 related to the invention.
XX KW Superantigen toxin; vaccine; infection; gene therapy.
XX OS Unidentified.
XX PN WO2003056015-A1.
XX PD 10-JUL-2003.
XX PF 26-NOV-2001; 2001WO-US046540.
XX PR 26-NOV-2001; 2001US-00002784.
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PI ULRICH RG;
XX WPI; 2003-492125/46.
XX DR N-PSDB; RAD56764.
XX New superantigen toxin DNA fragment, useful for preparing a composition for treating or preventing bacterial infection.
XX Disclosure; Page 108-109; 141pp; English.

XX The invention provides a superantigen toxin DNA fragment which has been genetically altered such that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is disrupted or altered. DNA fragments of the invention are useful in the production of CC vaccines against bacterial superantigen toxin infections. They are also CC useful in gene therapy. The present sequence is a protein related to the CC invention
XX SQ Sequence 257 AA;


```

Query Match      80.8%; Score 1000; DB 7; Length 257;
Best Local Similarity 80.7%; Pred. No. 7.2e-92;
Matches 188; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLT 144
QY 121 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 180
DB 145 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 204
QY 181 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENHLDLYLTT 233
DB 205 RGLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENHLDLYLTT 257

RESULT 34
AAY54463
ID AAY54463 standard; protein; 233 AA.
XX
AC AAY54463;
XX
DT 25-APR-2000 (first entry)
XX
DE Amino acid sequence of a mutant Staphylococcus enterotoxin A.
XX
KW Mutant; SEA gene; enterotoxin A; SEB gene; nucleic acid vaccine;
KW Venezuelan equine encephalitis virus; vaccine vector; vaccine;
KW Staphylococcus intoxication; Staphylococcus exotoxin.
XX
OS Staphylococcus aureus.
XX
FH Key Location/Qualifiers
FT Misc-difference 2 /note= "glu encoded by AGNA"
FT Misc-difference 4 /note= "Ser encoded by C"
XX
WO200002523-A2.
XX
PD 20-JAN-2000.
XX
PF 09-JUL-1999; 99WO-US015569.
XX
PR 10-JUL-1998; 98US-0092416P.
XX
PA (USMB-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX
XX Lee JS, Pushko P, Smith JF, Ulrich RG;
XX
XX WPI; 2000-160826/14.
XX
DR N-PSDB; AA245833.
XX
XX New DNA construct useful as vaccines against enterotoxins of
XX Staphylococcus aureus which causes gastrointestinal distress, or toxic
XX shock syndrome.
XX
PS Disclosure; Page 28; 30pp; English.
XX
XX The present sequence is represents a mutant Staphylococcus enterotoxin A.
XX It is encoded by a mutant SEA gene. The mutant gene product is unable to
XX bind to the MHC on T-cells, and so is non-toxic. Mutant SEA and SEB genes
XX were inserted into a Venezuelan equine encephalitis (VEE) replicon
XX vector, to produce vaccine vectors. The mutant gene product is unable to
XX bind to the MHC on T-cells, and so is non-toxic. Self-replicating RNA
XX derived from the recombinant VEE vectors can be used as a nucleic acid
XX vaccine, or to transfect cells along with RNA from helper plasmids. The
XX vaccine, or to transfect cells along with RNA from helper plasmids. The

recombinant proteins produced are used as vaccines for providing immunity
against Staphylococcus intoxication or as a diagnostic tool for detection
of Staphylococcus exotoxin. The transformed host cells are used to
analyse the effectiveness of drugs and agents which inhibit S. aureus
exotoxins or release of exotoxins. Infectious alpha-virus particles
comprising the mutant SEA or SEB genes are used for providing immunity
against Staphylococcus exotoxins by generating a protective immune
reaction in humans or animals. The vaccines are used to reduce disease
symptoms or reduce severity of disease caused by enterotoxins of S.
aureus
XX
SQ Sequence 233 AA;
Query Match      80.5%; Score 996; DB 3; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.6e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;

QY 2 EKSEINEKDLRKSELOALNSLNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
DB 2 EKSEINEKDLRKSELOALNSLNRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDIDVYKGGKVDLYGAYGYOCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 181
DB 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVQ 181
QY 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENHLDLYLTT 233
DB 182 GLIVFHTSTEPSVNYDLFGAQQYSNTLLRIYRDNKTINSENHLDLYLTT 233

RESULT 35
ABB79502
ID ABB79502 standard; protein; 233 AA.
XX
AC ABB79502;
XX
DT 23-SEP-2002 (first entry)
XX
DE Staphylococcus enterotoxin A vaccine, cytoplasmic (A489270C).
XX
KW Enterotoxin A; superantigen; antigen; toxin; vaccine; A489270C;
KW attenuation; mutant; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 1 /note= "encoded by AT, apparent frameshift"
FT Misc-difference 48 /note= "wild-type Leu substituted by Arg"
FT Misc-difference 70 /note= "wild-type Asp substituted by Arg"
FT Misc-difference 92 /note= "wild-type Tyr substituted by Ala"
XX
US6399332-B1.
XX
PD 04-JUN-2002.
XX
PF 01-SEP-1998; 98US-00144776.
XX
XX 25-JUN-1997; 97US-00882431.
XX
XX (USSA ) US SEC OF ARMY.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2002-546281/58.
```

DR N-PSDB; ABN84223.
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX
 PS Claim 5; Col 37-39; 46pp; English.
 XX
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin A (SEA) vaccine, cytoplasmic (A489270C). The vaccine
 CC comprises 3 amino acid substitutions introduced into the SEA sequence:
 CC L48R, Y89A and D70R. These mutations reduce the binding of the toxin to
 CC major histocompatibility complex (MHC) Class II and/or T cell receptors.
 CC The protein is expressed as a nonsecreted product within host *Escherichia*
 CC *coli* cells. The vaccine is used to protect against superantigen toxin
 CC infections. Superantigen attributes are absent, but the superantigen is
 CC effectively recognised by the immune system and an appropriate antibody
 CC response is produced. In examples from the invention, attenuated
 CC superantigen toxins were shown to protect animals against challenge
 CC wild-type toxin. Methods of producing and using the altered superantigen
 CC toxins as vaccines, and in diagnosis and therapy, are provided. A
 CC multivalent vaccine consisting of altered superantigen toxins from SEA,
 CC SEB, SEC-1, TSS1-1 and streptococcal SPEA is predicted to provide
 CC protective immunity against the majority of bacterial superantigen toxins
 XX
 SQ Sequence 233 AA;
 Query Match 80.5%; Score 996; DB 5; Length 233;
 Best Local Similarity 80.6%; Pred. No. 1.6e-91;
 Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
 DB 2 EKSEINEKDLRKSELQGTALGNLQIYYNEKAKTENKESHQFRHTILFKGFFTDH 61
 QY 62 PWYNDLLVGLSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKQIVDKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVOR 181
 DB 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNYNSDVFQKQVOR 181
 QY 182 GLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDIYLTS 233
 RESULT 36
 ABU10082
 ID ABU10082 standard; protein; 233 AA.
 XX
 AC ABU10082;
 XX
 XX 11-AUG-2003 (first entry)
 DT
 DE Staphylococcal enterotoxin A #2.
 XX
 KW Enterotoxin A; superantigen-associated bacterial infection; vaccine;
 KW superantigen toxin.
 XX
 OS Staphylococcus sp.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1
 FT /note= "Encoded by AT"
 XX
 PN US2003009015-A1.
 XX
 XX 09-JAN-2003.
 PD
 XX 25-JUN-1997; 97US-00882431.
 XX

PR 25-JUN-1997; 97US-00882431.
 XX (ULRI/) ULRICH R. G.
 PA (OLSO/) OLSON M. A.
 PA (BAVA/) BAVARI S.
 XX
 PI Ulrich RG, Olson MA, Bavari S;
 XX
 XX WPI: 2003-401542/38.
 DR N-PSDB; ACA61178.
 XX
 PT New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX
 PS Claim 11; Page 20-21; 50pp; English.
 XX
 CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of staphylococcal enterotoxin
 CC A #2
 XX
 SQ Sequence 233 AA;
 Query Match 80.5%; Score 996; DB 6; Length 233;
 Best Local Similarity 80.6%; Pred. No. 1.6e-91;
 Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGH 61
 DB 2 EKSEINEKDLRKSELQGTALGNLQIYYNEKAKTENKESHQFRHTILFKGFFTDH 61
 QY 62 PWYNDLLVGLSKDATNKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKQIVDKYKGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYNSDSFGKQVOR 181
 DB 122 EKKVPINLWIDGKQNTVPLETVTKNKNVTVOELDLQARRYLQEKYNYNSDVFQKQVOR 181
 QY 182 GLIVFHSSEGSVSYDLFDAQGYPTLLRIYRDNKTINSENHLDLYLTT 233
 DB 182 GLIVFHTSTEPSVNYDLFGAQGYNTLLRIYRDNKTINSENHLDIYLTS 233
 RESULT 37
 ABU62325
 ID ABU62325 standard; protein; 233 AA.
 XX
 AC ABU62325;
 XX
 XX 27-AUG-2003 (first entry)
 DT
 DE *S. aureus* cytoplasmic enterotoxin A mutant #1.
 XX
 KW SEA; staphylococcal enterotoxin A; mutein; mutant; vaccine;
 KW superantigen toxin; MHC; superantigen-associated bacterial infection;
 KW bacterial infection; antibacterial.
 XX
 OS Staphylococcus aureus.
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Misc-difference 1.2
 FT

FT Misc-difference 42 /note= "Encoded by ATGAG"
FT Misc-difference 48 /note= "Wild-type Leu substituted by Glu"
FT Misc-difference 48 /note= "Wild-type Leu substituted by Arg"
FT Misc-difference 70 /note= "Wild-type Asp substituted by Arg"
FT Misc-difference 89 /note= "Wild-type Tyr substituted by Gly"
FT Misc-difference 92 /note= "Wild-type Tyr substituted by Ala"
XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-00144776.
XX (ULRI/) ULRICH R G.
XX ULRICH RG;
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28895.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 24-25; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection, an
XX antiserum isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the L42E/L48R/D70R/Y89G/Y92A mutant of cytoplasmic
XX SEA
XX
SQ Sequence 233 AA;
Query Match 80.5%; Score 996; DB 7; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.6e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
DB 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
QY 62 PWYNDLLVGLSGKDAATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWDGKQNTVPLETVKTNKQNTVQVELDQARHYLHGKFGLYNSDSFGKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 182 GLIVFHTSTEPSVNDLFGAQOQYSNTLLRIYRDNKTINSENHLDLYLYTS 233

DB 182 GLIVFHTSTEPSVNDLFGAQOQYSNTLLRIYRDNKTINSENHLDLYLYTS 233
RESULT 38
AAE37677
ID AAE37677 standard; protein; 233 AA.
XX AAE37677;
XX 06-OCT-2003 (first entry)
XX Protein #2 related to the invention.
XX Superantigen toxin; vaccine; infection; gene therapy.
XX Unidentified.
XX Key Location/Qualifiers
FT Misc-difference 1 /note= "Encoded by AT"
XX WO2003056015-A1.
XX 10-JUL-2003.
XX 26-NOV-2001; 2001WO-US046540.
XX 26-NOV-2001; 2001US-00002784.
XX (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX ULRICH RG;
XX WPI; 2003-492125/46.
XX N-PSDB; AAD56765.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Page 110-112; 141pp; English.
XX The invention provides a superantigen toxin DNA fragment which has been
XX genetically altered such that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is disrupted or
XX altered. DNA fragments of the invention are useful in the production of
XX vaccines against bacterial superantigen toxin infections. They are also
XX useful in gene therapy. The present sequence is a protein related to the
XX invention
XX
SQ Sequence 233 AA;
Query Match 80.5%; Score 996; DB 7; Length 233;
Best Local Similarity 80.6%; Pred. No. 1.6e-91;
Matches 187; Conservative 17; Mismatches 28; Indels 0; Gaps 0;
QY 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
DB 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGH 61
QY 62 PWYNDLLVGLSGKDAATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
DB 62 SWYNDLLVRFDSKDI VDKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTE 121
QY 122 EKKVPINLWDGKQTTVPIDKVTSKKEVTQVELDQARHYLHGKFGLYNSDSFGKQVOR 181
DB 122 EKKVPINLWDGKQNTVPLETVKTNKQNTVQVELDQARHYLHGKFGLYNSDSFGKQVOR 181
QY 182 GLIVFHSSEGSTVSYDLFDAQGQYPTLLRIYRDNKTINSENHLDLYLYTT 233
DB 182 GLIVFHTSTEPSVNDLFGAQOQYSNTLLRIYRDNKTINSENHLDLYLYTS 233

RESULT 39
 ID ABU10099 standard; protein; 233 AA.
 XX AC ABU10099;
 XX DT 11-AUG-2003 (first entry)
 XX DE Staphylococcus enterotoxin A K14E substitution mutant.
 XX KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
 XX KW superantigen toxin; vaccine; mutein.
 XX OS Staphylococcus sp.
 XX OS Synthetic.
 XX FT Key Location/Qualifiers
 FT Misc-difference 14
 FT /note= "Wild-type Lys substituted by Glu"
 XX PN US2003009015-A1.
 XX PD 09-JAN-2003.
 XX PF 25-JUN-1997; 97US-00882431.
 XX PR 25-JUN-1997; 97US-00882431.
 XX PA (ULRI/) ULRICH R G.
 XX PA (OLSO/) OLSON M A.
 XX PA (BAVA/) BAVARI S.
 XX PI Ulrich RG, Olson MA, Bavari S;
 XX DR WPI; 2003-401542/38.
 XX PT New superantigen toxin and/or DNA fragment with an altered binding of the
 PT encoded altered toxin to either MHC class II or T cell antigen receptor,
 PT useful for treating or ameliorating superantigen-associated bacterial
 PT infection.
 XX PS Example 7; Page; 50pp; English.
 XX CC The invention relates to an isolated and purified superantigen toxin
 CC and/or DNA fragment, which has been altered so that the binding of the
 CC encoded toxin to either major histocompatibility complex (MHC) class II
 CC or T cell antigen receptor is altered. The superantigen toxins, DNA
 CC fragments, and vaccines are useful for treating or ameliorating
 CC superantigen-associated bacterial infection. The DNA fragments are
 CC particularly useful for producing vaccine against superantigen toxin
 CC infections. The transformed host cells are useful for analysing the
 CC effectiveness of drugs and agents that affect the binding of
 CC superantigens to MHC class II or T-cell antigen receptors. The present
 CC sequence represents the amino acid sequence of the staphylococcus
 CC enterotoxin A K14E mutant. Note: The present sequence is not present in
 CC the specification but was created by the indexer from the wild-type
 CC staphylococcus enterotoxin A sequence (see ACA61178)
 XX SQ Sequence 233 AA;
 Query Match 80.1%; Score 992; DB 6; Length 233;
 Best Local Similarity 80.2%; Pred. No. 4e-91;
 Matches 186; Conservative 18; Mismatches 28; Indels 0; Gaps 0;
 QY 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
 DB 2 EKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 61
 QY 62 PNYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 121
 DB 62 SWYNDLLVRFDSKQIVDYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLTE 121
 QY 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQVR 181

Db 122 EKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYNSDSFGKQVR 181
 QY 182 GLIVFHSSEGSTVSVDLFDAGQGYPDTLRLRIYRDNKTINSNLHLDLYLTT 233
 Db 182 GLIVFHTSTEPSVNDLFDAGQGYNSNTLLRLIYRDNKTINSNMHIDIYLYTS 233
 RESULT 40
 ADF89824
 ID ADF89824 standard; protein; 231 AA.
 XX AC ADF89824;
 XX DT 26-FEB-2004 (first entry)
 XX DE Staphylococcal enterotoxin A (SEA) superantigen.
 XX KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEA; cytostatic;
 XX KW gene therapy; cancer.
 XX OS Staphylococcus sp.
 XX PN WO2003094846-A2.
 XX PD 20-NOV-2003.
 XX PF 08-MAY-2003; 2003WO-US014381.
 XX PR 08-MAY-2002; 2002US-0378988P.
 XX PR 15-JUN-2002; 2002US-0389366P.
 XX PR 28-AUG-2002; 2002US-0406697P.
 XX PR 29-AUG-2002; 2002US-0406750P.
 XX PR 01-OCT-2002; 2002US-0415310P.
 XX PR 02-OCT-2002; 2002US-0415400P.
 XX PR 09-JAN-2003; 2003US-0438686P.
 XX (TERM/) TERMAN D S.
 XX Terman DS;
 XX WPI; 2004-011997/01.
 XX PT Treating a subject with cancer or malignant diseases comprises
 PT intratumoral, intrathecal or intracavitary administration of an amount of
 PT a superantigen composition to the subject.
 XX PS Disclosure; SEQ ID NO 1; 91pp; English.
 XX CC The invention relates to treating a subject with cancer. The method
 CC involves administering an amount of a superantigen (SAG) composition
 CC comprising a molecule selected from: a native SAG protein; its
 CC biologically active fragment or a biologically active homologue or a
 CC biologically active fusion protein comprising the SAG or its fragment or
 CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
 CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
 CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritides SAG and
 CC Clostridium perfringens exotoxin. The method is useful in treating cancer
 CC or malignant diseases such as malignant pleural effusion, ascites,
 CC pericardial effusion or meningeal carcinomatosis. The present sequence
 CC represents a Staphylococcal enterotoxin A (SEA) superantigen.
 XX SQ Sequence 231 AA;
 Query Match 80.0%; Score 991; DB 8; Length 231;
 Best Local Similarity 80.3%; Pred. No. 5e-91;
 Matches 187; Conservative 18; Mismatches 26; Indels 2; Gaps 1;
 QY 1 SEKSEINEKDLRKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
 Db 1 SEKSEINEKDLRKSELQNGTA--GNKQIYYNEKAITENKESDDQFLENTLLFKGFFTG 58
 QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTENKTACMYGGVTLHDNNRLT 120

Db 59 HSWYNDLLVDFDSKDI VDKYKGGKVDLYGAYGYQCAGT PNTKACMYGGVTLHDNNRLT 118
Qy 121 EKKKVPINLWIDGKOTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 119 EKKKVPINLWIDGKONTVPLETVTKNKNTVOELDLQARRYLQEKYKLYNSDVPDGVQ 178
Qy 181 RGLIVFHSSEGSTSVSYDLFDAGQYPTDLLRIYRDNKTINSNLHIDLYTT 233
Db 179 RGLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKINSNMHIDIYLYTS 231
RESULT 41
ABU10098
ID ABU10098 standard; protein; 233 AA.
XX
AC ABU10098;
XX
DT 11-AUG-2003 (first entry)
XX Staphylococcus enterotoxin A Y64A substitution mutant.
DE
XX
KW Enterotoxin A; superantigen-associated bacterial infection; mutant;
KW superantigen toxin; vaccine; mutein.
XX
OS Staphylococcus sp.
OS Synthetic.
XX
XX
FH Key Location/Qualifiers
FT Misc-difference 64 /note= "Wild-type Tyr substituted by Ala"
FT
XX
XX
PN US2003009015-A1.
XX
XX
PD 09-JAN-2003.
XX
XX
PF 25-JUN-1997; 97US-00882431.
XX
PR 25-JUN-1997; 97US-00882431.
XX
XX (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
XX
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2003-401542/38.
XX
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX
XX Example 7; Page; 50pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of the staphylococcus
CC enterotoxin A Y64A mutant. Note: The present sequence is not present in
CC the specification but was created by the indexer from the wild-type
CC staphylococcus enterotoxin A sequence (see ACA61178)
XX
SQ Sequence 233 AA;
Query Match 79.7%; Score 987; DB 6; Length 233;

Best Local Similarity 80.2%; Pred. No. 1.3e-90;
Matches 186; Conservative 17; Mismatches 29; Indels 0; Gaps 0;
Qy 2 EKSEINEKDLRKSELOQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 2 EKSEINEKDLRKSELOQNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Qy 62 PWYNDLLVDSKDATNKYKGGKVDLYGAYGYQCAGT PNTKACMYGGVTLHDNNRLTE 121
Db 62 SWANDLLVRFDSKDI VDKYKGGKVDLYGAYGYQCAGT PNTKACMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKOTTPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSDSFGGKVQ 181
Db 122 EKKVPINLWIDGKONTVPLETVTKNKNTVOELDLQARRYLQEKYKLYNSDVPDGVQ 181
Qy 182 GLIVFHSSEGSTSVSYDLFDAGQYPTDLLRIYRDNKTINSNLHIDLYTT 233
Db 182 GLIVFHTSTEPSVNYDLFGAQGYSTNLLRIYRDNKINSNMHIDIYLYTS 233
RESULT 42
AAV70102
ID AAV70102 standard; protein; 257 AA.
XX
AC AAV70102;
XX
DT 05-JUN-2000 (first entry)
XX
XX Staphylococcal enterotoxin A.
DE
XX
KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis;
KW treatment; superantigen-associated bacterial infection.
XX
OS Staphylococcus sp.
XX
FH Key Location/Qualifiers
FT Peptide 2..25 /label= Leader_peptide
FT Protein 26..253
FT /label= Mature Staphylococcal enterotoxin A
FT /note= "Includes transcription start site residue, Met"
FT Misc-difference 42 /note= "Encoded by TTG"
FT Misc-difference 125 /note= "Encoded by CCA"
FT
XX WO200009154-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1998; 98WO-US016766.
XX
XX 13-AUG-1998; 98WO-US016766.
XX (REED-) REED ARMY INST RES WALTER.
XX
XX Ulrich RG, Olson MA, Bavari S;
XX
XX WPI; 2000-224177/19.
XX N-PSDB; AA251105.
XX
XX Nucleic acid encoding superantigen toxin useful as a vaccine and for
PT diagnosis of superantigen-associated bacterial infections.
XX
XX Claim 7; Page 72-73; 118pp; English.
XX
XX The present amino acid sequence is the Staphylococcal enterotoxin A
CC (SEA), a bacterial superantigen toxin (SAG). The coding region of the SAG
CC toxin when altered by site directed mutagenesis, results in disruption of
CC binding of the toxin to both the MHC class II or T-cell antigen receptor.
CC SEA has antibacterial and cytostatic activity. This sequence is useful

CC for the production of SEA vaccines and specific antibodies. This vaccine
CC overcomes the disadvantages of the chemically inactivated toxoids and is
CC designed to protect individuals against one or several related
CC staphylococcal and streptococcal toxins. It is used for the diagnosis and
CC treatment or amelioration of superantigen- associated bacterial
CC infections
XX
SQ Sequence 257 AA;

Query Match 79.4%; Score 983; DB 3; Length 257;
Best Local Similarity 79.8%; Pred. No. 3.7e-90;
Matches 186; Conservative 17; Mismatches 30; Indels 0; Gaps 0;

Qy 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTG 60
Db 25 SEKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESDDQFQHTILPKGFTD 84
Qy 61 HPWYNDLLVLDGSKDNTNKKYKGVVLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVRFDSKDI VDKYKGVVLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLT 144
Qy 121 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKQV 180
Db 145 EEKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKQV 204
Qy 181 RGLIVFHTSTSPSVNYDLFGAQGGYNTLLRIYRDNKTINSENHIDLILYLYTT 233
Db 205 RGLIVFHTSTSPSVNYDLFGAQGGYNTLLRIYRDNKTINSENHIDLILYLYTS 257

RESULT 43
AAAY70103
ID AAAY70103 standard; protein; 233 AA.
XX
AC AAAY70103;
XX
DT 05-JUN-2000 (first entry)
XX
DE Mutant Staphylococcal enterotoxin A for vaccine A489270P.
XX
KW Superantigen toxin; SAG; Staphylococcal enterotoxin A; SEA; cytostatic;
KW antibacterial; vaccine; MHC class II receptor; T-cell antigen receptor;
KW antibody; toxoid; staphylococcal/streptococcal toxin; diagnosis; mutant;
KW treatment; superantigen-associated bacterial infection; A489270P.
XX
OS Staphylococcus sp.

XX Key Location/Qualifiers
FH 1. .233
FT Protein /label= Mature Staphylococcal enterotoxin A
FT /note= "Mutant" sequence without the leader peptide"
FT Misc-difference 2 /note= "Encoded by AG"
FT Misc-difference 18 /note= "Encoded by TTG"
FT Misc-difference 48 /note= "Wild type Leu substituted with Arg"
FT Misc-difference 70 /note= "Wild type Asp substituted with Arg"
FT Misc-difference 92 /note= "Wild type Tyr substituted with Ala"
FT Misc-difference 157 /note= "Encoded by CTT"
FT Misc-difference 180 /note= "Encoded by CAG"

XX WO200009154-A1.
XX
XX 24-FEB-2000.
XX
XX 13-AUG-1998; 98WO-US016766.
XX
XX 13-AUG-1998; 98WO-US016766.

XX
PA (REED-) REED ARMY INST RES WALTER.
XX
PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2000-224177/19.
DR N-PSDB; AAZ51106.
XX
PT Nucleic acid encoding superantigen toxin useful as a vaccine and for
FT diagnosis of superantigen-associated bacterial infections.
XX
PS Claim 8; Page 74-76; 118pp; English.
XX
CC The present amino acid sequence is the mutant Staphylococcal enterotoxin
CC A (SEA), a bacterial superantigen toxin (Sag), used for the formulation
CC of SEA vaccine A489270P. The coding region of this Sag toxin is altered
CC by site directed mutagenesis, that results in disruption of binding of
CC the toxin to both the MHC class II or T-cell antigen receptor. This
CC altered Sag toxin has the leader peptide cleaved by native bacterial
CC enzymatic mechanism and the first residue of the mature protein is
CC encoded by the transcriptional start site (ATG). SEA has antibacterial
CC and cytostatic activity. This sequence is useful for the production of
CC SEA vaccines and specific antibodies. This vaccine overcomes the
CC disadvantages of the chemically inactivated toxoids and is designed to
CC protect individuals against one or several related staphylococcal and
CC streptococcal toxins. It is used for the diagnosis and treatment or
CC amelioration of superantigen-associated bacterial infections
XX
SQ Sequence 233 AA;

Query Match 79.0%; Score 978; DB 3; Length 233;
Best Local Similarity 79.3%; Pred. No. 1e-89;
Matches 184; Conservative 17; Mismatches 31; Indels 0; Gaps 0;
Qy 2 EKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTGH 61
Db 2 EKSEINEKDLRKSEKQGTALGNLQIYYNEKAITENKESDDQFQHTILPKGFTDH 61
Qy 62 PWYNDLLVLDGSKDNTNKKYKGVVLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Db 62 SWYNDLLVRFDSKDI VDKYKGVVLYGAYGYQCAGTGNKTCMYGGVTLHDNNRLTE 121
Qy 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKQV 181
Db 122 EKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHYLHGKGLYNSDSFGKQV 181
Qy 182 GLIVFHTSTSPSVNYDLFGAQGGYNTLLRIYRDNKTINSENHIDLILYLYTT 233
Db 182 GLIVFHTSTSPSVNYDLFGAQGGYNTLLRIYRDNKTINSENHIDLILYLYTS 233

RESULT 44
ADF89835
ID ADF89835 standard; protein; 268 AA.
XX
AC ADF89835;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin J (SEJ) superantigen.
XX
KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEJ; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
XX WO2003094846-A2.
XX
XX 20-NOV-2003.
XX
XX 08-MAY-2003; 2003WO-US014381.
XX
XX 08-MAY-2002; 2002US-0378988P.

Best Local Similarity 54.5%; Pred. No. 6e-58;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY

1 SEKSEENEKDLRKKSELQRNALSNLRQIYYVNEKAITENKESDDQLFENTLLFKGPFPTG 60
 :
 :

Db

26 NENIDSVKELHKKSLSLTALNMKHVSADKNPIGENKSTGDQFLNTLLLYKCFPTD 85
 :
 :

QY

61 HPWYNDDLVLGSKDATNKGKVVDLGYGVYCAGGTGNKTACMYGGVTTLHDNNRLT 120
 :
 :

Db

86 LINFNSLKEMAHFKSKNDVVPIRSINCYSGEIDRTACTYGCVTPHEGKCLK 145
 :
 :

QY

121 EEKVVPNLWDIGQTTPFDIKVTSKEVTVQBLDAQRYHLHGKGLYSDFSFGKVQ 180
 :
 :

Db

146 ERKIIPNLWMINGVQEVSLEDKVTDKNVTVBELDAQARYLOKDLKLNNDTLGSKIQ 205
 :
 :

QY

181 RGLIVPSSSEGSTSVYLFDAOGVOYPDTLLRIYRDNKTTINSENLHIDLILY 231
 :
 :

Db

206 RGKIEFUSSDGSKSYLDLFVKGFPEPKQLRIYSDNKTSLSTEHLHIIDIYLY 256
 :
 :

RESULT 46

ADF43294

ID ADF43294 standard; protein; 258 AA.

AC ADF43294;

XX XX

12-FEB-2004 (first entry)

XX XX

Staphylococcal enterotoxin D polypeptide seq id 14.

DE XX

receptor; lipid-based tumour associated antigen; cytostatic;
KW antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW infectious disease; Staphylococcal enterotoxin D; SED; enterotoxin D.
XX XX

OS Staphylococcus.

XX XX

US2003157113-A1.

XX XX

21-AUG-2003.

XX XX

28-DEC-2000; 2000US-00751708.

PF XX

28-DEC-1999; 99US-0173371P.

PR XX

(TERM/) TERMAN D S.

PA XX

Terman DS;

PI XX

WPI; 2003-787326/74.

DR XX

New receptor in a mammalian cell that inhibits regular activation by
PT receptors specific for lipid-based tumor associated antigens, useful for
PT treating a neoplastic disease or tumor, and infectious diseases.

XX XX

Example 3; SEQ ID NO 14; 151bp; English.

PS PS

The invention describes a receptor in a mammalian cell that inhibits
CC regular activation by receptors specific for lipid-based tumour
CC associated antigen. The receptor has cytostatic and antimicrobial
CC properties and is suitable for use in gene therapy. The receptors,
CC methods and compositions are useful for treating a neoplastic disease or
CC tumour (cancer), and infectious diseases. This is the amino acid sequence
CC of an enterotoxin superantigen polypeptide the DNA encoding which can be
CC transfected in to a cell alone or with DNA encoding a cell surface moiety
CC to generate antitumour immunity.

XX XX

Sequence 258 AA;

SQ XX

Query Match 53.6% ; Score 663; DB 7; Length 258;

Best Local Similarity 54.5%; Pred. No. 6e-58;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY

1 SEKSEENEKDLRKKSELQRNALSNLRQIYYVNEKAITENKESDDQLFENTLLFKGPFPTG 60
 :
 :

	Best Local Similarity	54.5%	Pred.No. 6e-59;	Mismatches	70;	Indels	0;	Gaps	0;
	Matches	126;	Conservative	35;					
y	1	SEKSEINEKDLURKXSEIQRNALSNLROIYYNEKAITENKESDDQFLENTLLPKGPTG	60						
b	26	NENIDSVKEKEHLKXSELSSLTANNMKHSYADKPNPIIGENKSTGDFLENTLLYKKPFTD	85						
y	61	HPWYNDLIVDLGSKDATNKYKGGKVDLYGAYVGYOCAGGTGNKTKACMYGGVTLHDNNRLT	120						
b	86	LINPEDLLINFNSKEMAQHFPSKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNKIK	145						
y	121	EEKKVPINLWDGKQTTPVIDKVTTSKEVTVQELDLQARHVLHGKFLGYNSSDFGKVQ	180						
b	146	ERKKIPINLIWNGVQRELSLDKQTDKGNVTVQELDAQRYLQKDLKNNDTLGGKIQ	205						
y	181	RGLIVFHSEGSTVSVDLPDAQGYPTDLLRIYDRNKTINSENLHIDLYL	231						
b	206	RKGIIFSDSDGSKSVYDFVDKVGDPPEKQIRIYSDNKTLSTEHLHIDLYL	256						

RESULT 48	
AR45013	
D	AAR45013 standard; protein; 228 AA.
X	
C	AAR45013;
X	
X	25-MAR-2003 (revised)
T	08-JUN-1994 (first entry)
T	
X	Staphylococcal enterotoxin SED.
E	
E	Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
X	autoimmune disease; toxicity; Protein A; perfusion system.
W	
W	
X	Staphylococcus aureus.
S	
S	WO9324136-A1.
X	
X	09-DEC-1993.
D	
X	01-JUN-1993; 93WO-US005213.
F	
P	01-JUN-1992; 92US-00891718.
R	
R	(TERM/) Terman D S.
X	(STON/) Stone J L.
A	
A	Terman DS, Stone JL;
X	
I	WPI; 1993-405418/50.
I	
X	Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
X	in a patient or for the treatment of auto-immune diseases.
T	
T	
X	Disclosure; Fig 1; 90pp; English.
X	
S	The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
X	which may be used in the methods of the invention for treating cancer in
C	a patient. These SEs, and homologues of them, can be used as tumouricidal
C	agents for treating cancers and autoimmune disease. They exhibit
C	tumouricidal activity and toxicity identical to that observed for the
C	Protein A perfusion system. They may be administered by i.v. injection.
C	(Updated on 25-MAR-2003 to correct PN field.)
C	
C	Sequence 228 AA;
X	

```

Query Match      53.1%; Score 657; DB 2; Length 228;
Best Local Similarity 55.6%; Pred. Mo. 2e-57;
Matches 125; Conservative 33; Mismatches 67; Indels 0; Gaps 0

          7 INEKDKRKSELORNLSNRQIYYNNEKAITENKESDDQFLNTILFKGFFTHGHPWYND 66
          2 VKEKELHKKSELSTLNNMKHSYADKNPIIGENKSTGDOFLNTILLYKKFPTDLINFD 61

```

Qy	67	LLVLDGSDATNWKYKKKVDLXGAYYGCAGGTPNKATCMYGGVTLHDNNRLTEEEKVP	126
Db	62	LLINFSKEMAQHFSKKNVDVPIRYISNCVGGIDRIATYIGVTPHEGNKKERKVP	121
Qy	127	INLWIDGQGTTPVDPKVTKSKKVTYVQELDLQARHYLHGKGLYNSDSFGCKVQRGILVF	186
Db	122	INLWINGVQKEVSLDKVQTDKXNTYVQELDAQARYYLQKDLKLYNNDTLGGKIQGKIEF	181
Qy	187	HSSEGSTVSYDLFAQGGQYPTLLRIYRDNKTINSENLIHIDLXYL	231
Db	182	DSSDGSKVSYDLFDVKGGDFPEKQRIYSDNKTILSTEHLLHIDLXYL	226

RESULT 49	
AAB67340	
ID	AAB67340 standard; peptide; 228 AA.
XX	
AC	AAB67340;
XX	
XX	
DT	23-APR-2001 (first entry)
XX	
DE	Staphylococcus aureus enterotoxin D protein.
XX	
KW	Tumour; cancer; immune; enterotoxin.
XX	
XX	
OS	Staphylococcus aureus.
XX	
PN	US6180097-B1.
XX	
PD	30-JAN-2001.
XX	
PF	30-OCT-1998; 98US-00183437.
XX	
PR	03-OCT-1989; 89US-00416530.
PR	17-JAN-1990; 90US-00466577.
PR	17-JAN-1991; 91WO-US0000342.
PR	01-JUN-1992; 92US-00891718.
PR	02-MAR-1993; 93US-00025144.
PR	31-JAN-1994; 94US-00189424.
PR	19-JUN-1995; 95US-00491746.
XX	
PA	(TERM/) TERMAN D S.

XX Terman DS;
XX
XX WPI; 2001-158657/16.
XX
XX Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX
XX Disclosure; Fig 2; 16pp; English.
XX
XX The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX
XX Sequence 228 AA;
XX SQ

```
Query Match      53.1%; Score 657; DB 4; Length 228;  
Best Local Similarity    55.6%; Pred. No. 2e-57;  
. Matches 125; Conservative 33; Mismatches 67; Indels   0; Gaps  
  
QY       7 INEKDLKKSEIQRNALSRLRIYYNEKAITENKSDQFLENTLLPKGFTGHYPWND 66  
Db        2 VKEIKLHKSSLSIALNNKHESYADKNPIIGENCSTGDPLENLTLYKYFFDILINFED 61  
  
QV       67 LLVDLGSKDATNKYGKKGVLDLYCAYGYQCAGTNPKTACMGVTLHNNRNLTEEEKVP 12
```


Db 2 VKEKELHKKSLSSTALNNMKHSYADNP I I GENKSTGDFLENTLLYKKFTDILNFED 61
 QY 67 LLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTGNKTACTMGTGGVTLHDNNRLTEKKVP 126
 Db 62 LLINFSKEMAQHFESKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIP 121
 QY 127 INLWIDGKTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVF 186
 Db 122 INLWINGVQKESLDKVDQKKNVTQELDLQARRYLQKDLKLYNNDTLGGKIQRGKIEF 181
 QY 187 HSEGSTVSVDLFDAGQVPTLLRIYRDNKTINSENHLHIDLVL 231
 Db 182 DSSDGSKVSVDLFDVKGDFPEKQLRIYSDNKTLSLHHLHIDLVL 226

RESULT 52

ABP58459
 ID ABP58459 standard; protein; 203 AA.

XX AC ABP58459;
 XX 14-APR-2003 (first entry)
 XX Staphylococcal enterotoxin D.
 DE Superantigen; staphylococcal enterotoxin D; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 XX Staphylococcus sp.
 OS WO2003002143-A1.
 PN 09-JAN-2003.
 PD 19-JUN-2002; 2002WO-SE001188.
 PF 28-JUN-2001; 2001SE-00002327.
 PR (ACTI-) ACTIVE BIOTECH AB.
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 XX WPI; 2003-201467/19.

DR Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 PS Example 3; Fig 3; 102pp; English.
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin D (SED). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)

XX Sequence 203 AA;
 Query Match 42.2%; Score 523; DB 6; Length 203;
 Best Local Similarity 49.5%; Pred. No. 5.2e-44;
 Matches 109; Conservative 25; Mismatches 66; Indels 20; Gaps 3;
 QY 12 LRKSELOALNRLRQIYYNEKAITENKESDDQFLENTLLKGGPTGHPWINDLVL 71
 Db 2 LHKKSELSALNNMKHSYADNP I I GENKSTGDFLENTLLYKKFTDILNF 53

QY 72 GSKDATNKYKGGKVDLYGAYYGOCAGTGNKTACTMGTGGVTLHDNNRLTEKKVPINLWI 131
 Db 54 NSAEHAQHFESKNVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKERKKIPINLWI 107
 QY 132 DGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEG 191
 Db 108 IGQXEVSLDKVDQKKNVTQELDLQARRYLQKDLKLYNA-----IQRGKLEFDSAAA 161
 QY 132 STVSVDLFDAGQVPTLLRIYRDNKTINSENHLHIDLVL 231
 Db 162 SKVSVDLFDVAGDFPEKQLRIYSDNKTLSLHHLHIDLVL 201

RESULT 53

ABM70958
 ID ABM70958 standard; protein; 250 AA.

XX AC ABM70958;
 XX 20-NOV-2003 (first entry)
 XX Staphylococcus aureus protein #198.
 DE Antibacterial; vaccine; gene therapy; infection; sepsis; diagnosis;
 KW enzymatic assay; antibiotic target.
 XX Staphylococcus aureus.
 OS WO200294868-A2.
 PN 28-NOV-2002.
 PD 27-MAR-2002; 2002WO-IB002637.
 PF 27-MAR-2001; 2001GB-00007661.
 PR (CHTR-) CHIRON SPA.
 XX Masignani V, Mora M, Scarselli M;
 XX WPI; 2003-120786/11.
 DR N-PSDB; ACF72518.
 XX New Staphylococcus aureus protein, useful as a vaccine for treating or
 PT preventing Staphylococcal infection, specifically an infection caused by
 PT S. aureus, e.g. sepsis.
 XX Claim 1; SEQ ID NO 396; 49pp; English.

XX The invention relates to novel genes and encoded proteins from
 CC Staphylococcus aureus. A composition comprising the S. aureus protein, a
 CC nucleic acid encoding the protein, or an antibody to the protein, is
 CC useful as a pharmaceutical, particularly as a vaccine for treating or
 CC preventing infection due to Staphylococcus bacteria, specifically an
 CC infection caused by S. aureus. The composition is particularly useful for
 CC treating or preventing sepsis in a patient. The composition can also be
 CC used for diagnostics. The protein is also used in an assay for enzymatic
 CC studies and as a target for antibiotics. This sequence represents one of
 CC the novel S. aureus proteins of the invention

XX Sequence 250 AA;

Query Match 39.8%; Score 492.5; DB 6; Length 250;
 Best Local Similarity 39.8%; Pred. No. 8.3e-41;
 Matches 92; Conservative 48; Mismatches 86; Indels 5; Gaps 3;

QY 1 SEKSEINERKDRKKSELOALNRLRQIYYNEKAITENKESDDQFLENTLLKGGFTG 60
 Db 23 TNSASAIETSYDLHHSKFDPSKRLSNAK-MSFINPTQL-ENKNTNDRLLKHLHDFDMFVN 80
 QY 61 HPWINDLVLGSKDQATNKYKGGKVDLYGAYYGOCAGTGNKTACTMGTGGVTLHDNNRLT 120
 Db 81 DDKKDFKVEFENEALSKKPIINKIDIFAGNYGCHGGATNKTQCSYGGVTLSDNNKYD 140

Qy 121 BEKKVPINIWIDCKQTTPYDIPDKVTKTSKEVTVOELDIQARHYLHGKGLNSDSFGGKVQ 180

Db 141 DYKNIPCNWIDGHOTHEIETLTAVTKYKXIVITIOEVLQNLYNLEKYKJYEQ---GGDIV 197

Qy 181 RGLIVPHSSEGSTVSVDLFDAQOQPDTLLRIYDRNKNTINSENLIHLIYL 231

Db 198 KGVKYKYNDEONVEYDFVNLNGEXGRELVKMYADKNTSDSKLHLDIYF 248

RESULT 54
ABU10091
ID ABU10091 standard; protein; 82 AA.
XX
XX ABU10091;
XX AC
XX AC
XX 11-AUG-2003 (first entry)
XX
XX Bacterial superantigen toxin SEE.
DE
XX
XX Superantigen-associated bacterial infection; superantigen toxin; vaccine;
KW
KW SEE.

XX	Unidentified.
OS	
XX	
PN	US2003009015-A1.
XX	
PD	09-JAN-2003.

PF	25-JUN-1997;	97US-00882431.
XX		
PR	25-JUN-1997;	97US-00882431.

PA (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.

PI Ulrich RG, Olson MA, Bavari S;
XX
DR WPI; 2003-401542/38.

PT New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.

Example 1; Page 36; 50pp; English.

The invention relates to an isolated and purified superantigen toxin and/or DNA fragment, which has been altered so that the binding of the encoded toxin to either major histocompatibility complex (MHC) class II or T cell antigen receptor is altered. The superantigen toxins, DNA fragments, and vaccines are useful for treating or ameliorating superantigen-associated bacterial infection. The DNA fragments are particularly useful for producing vaccine against superantigen toxin infections. The transformed host cells are useful for analysing the effectiveness of drugs and agents that affect the binding of superantigens to MHC class II or T-cell antigen receptors. The present sequence represents the amino acid sequence of the bacterial superantigen toxin SEB

SQ Sequence 82 AA; Query Match 36.9%; Score 457; DB 6; Length 82; Best Local Similarity 100.0%; Pred. No. 6.3e-38;

Qy	43	SDDOFLENTLLFKGFFTGHPWNDLLVLDGSKDATNKYKGKKVDLYGAYVGYQCAGGTPN	102
Dp	1	SDDOFLENTLLFKGFFTGHPWNDLLVLDGSKDATNKYKGKKMDYGAYVGYQCAGGTPN	60

Qy 103 KTACMYGGVTLHDNNRLTEKK 124

```

Db          61  KTCMYGGVTIHDNNRLTEKK 82

RESULT 55
ABU62338
ID      ABU62338 standard; protein; 82 AA.
XX
AC      ABU62338;
XX
XX      27-AUG-2003 (first entry)
XX
XX      S. aureus enterotoxin E, SEE, MHC binding region.
DE
DE      SEE; staphylococcal enterotoxin E; vaccine; superantigen toxin; MHC;
KW      superantigen-associated bacterial infection; bacterial infection;
KW      antibacterial.
XX
XX      Staphylococcus aureus.
OS
XX
XX      US2003036644-A1.
PN
XX
XX      20-FEB-2003.
PD
XX
XX      26-NOV-2001; 2001US-00002784.
XX
XX      25-JUN-1997; 97US-00882431.
PR
PR      01-SEP-1998; 98US-00144776.
XX
XX      (ULRI/) ULRICH R G.
FA
XX
XX      Ulrich RG;
XX
XX      WPI; 2003-492125/46.
XX
XX      New superantigen toxin DNA fragment, useful for preparing a composition
FT      for treating or preventing bacterial infection.
PS      Disclosure: Fig 3; 68pp; English.

```

The invention relates to an isolated and purified superantigen toxin DNA fragment is altered so that binding of the encoded altered toxin to either the MHC class II or T cell antigen receptor is altered. Also included are a recombinant DNA construct (comprising a vector and an isolated and purified altered superantigen toxin DNA fragment), a host cell transformed with the recombinant DNA construct, producing altered superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin) superantigen toxin peptide, diagnosing superantigen-associated bacterial infection, a vaccine (comprising an altered superantigen toxin for producing antigenic and immunogenic response resulting in the protection of a mammal against superantigen-associated bacterial infection), and treating/ameliorating a superantigen-associated bacterial infection, an antiserum isolated from individuals immunised with one or more altered TSST-1 superantigen toxin and an antibody which recognises altered TSST-1 superantigen toxin.

1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA, SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and SPEb). The superantigen toxin DNA fragment is useful for preparing a composition for treating or preventing bacterial infection. The present sequence represents the *S. aureus* enterotoxin E, SEE, MHC binding region

Sequence 82 AA:

Query Match 36.9%; Score 457; DB 7; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.3e-38;
Matches 82; Conservative 0; Mismatches 0; Indels 0; Gaps 0

Db 1 SDQFLENTLLFGGFFCTGHPWYNDLLVDLGSKDATNKYRGKKVDLYGAYYGYQCAGGTPN 60

Qv 103 KTACMYGGVTLDHNNRLTEKK 124

Db 61 KTACMYGGVTLHDNNRLTEKK 82

RESULT 56
ABU10089
ID ABU10089 standard; protein; 82 AA.
XX AC ABU10089;
XX DT 11-AUG-2003 (first entry)
XX DE Bacterial superantigen toxin SEA.
XX KW Superantigen-associated bacterial infection; superantigen toxin; vaccine;
XX OS Unidentified.
XX PN US2003009015-A1.
XX PD 09-JAN-2003.
XX PF 25-JUN-1997; 97US-00882431.
XX PR 25-JUN-1997; 97US-00882431.
XX PA (ULRI/) ULRICH R G.
XX PA (OLSO/) OLSON M A.
XX PA (BAVA/) BAVARI S.
XX PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
XX encoded altered toxin to either MHC class II or T cell antigen receptor,
XX useful for treating or ameliorating superantigen-associated bacterial
XX infection.
XX Example 1; Page 35; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
XX and/or DNA fragment, which has been altered so that the binding of the
XX encoded toxin to either major histocompatibility complex (MHC) class II
XX or T cell antigen receptor is altered. The superantigen toxins, DNA
XX fragments, and vaccines are useful for treating or ameliorating
XX superantigen-associated bacterial infection. The DNA fragments are
XX particularly useful for producing vaccine against superantigen toxin
XX infections. The transformed host cells are useful for analysing the
XX effectiveness of drugs and agents that affect the binding of
XX superantigens to MHC class II or T-cell antigen receptors. The present
XX sequence represents the amino acid sequence of the bacterial superantigen
XX toxin SEA
XX Sequence 82 AA;
Query Match 32.2%; Score 399; DB 6; Length 82;
Best Local Similarity 86.6%; Pred. No. 4.3e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 43 SDQQLFNTLLFKGFFTHGHPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTPN 102
DB 1 SHDQFLQHTILFKGFFTHGHPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTPN 60
QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82
RESULT 57
ABU62336
ID ABU62336 standard; protein; 82 AA.
XX AC ABU62336;
XX DT 14-APR-1998 (first entry)
XX

DT 27-AUG-2003 (first entry)
XX S. aureus enterotoxin A, SEA, MHC binding region.
XX SEA; staphylococcal enterotoxin A; vaccine; superantigen toxin; MHC;
XX superantigen-associated bacterial infection; bacterial infection;
XX antibacterial.
XX OS Staphylococcus aureus.
XX PN US2003036644-A1.
XX PD 20-FEB-2003.
XX PF 26-NOV-2001; 2001US-00002784.
XX PR 25-JUN-1997; 97US-00882431.
XX PR 01-SEP-1998; 98US-00144776.
XX PA (ULRI/) ULRICH R G.
XX PI Ulrich RG;
XX WPI; 2003-492125/46.
XX New superantigen toxin DNA fragment, useful for preparing a composition
XX for treating or preventing bacterial infection.
XX Disclosure; Fig 3; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
XX fragment is altered so that binding of the encoded altered toxin to
XX either the MHC class II or T cell antigen receptor is altered. Also
XX included are a recombinant DNA construct (comprising a vector and an
XX isolated and purified altered superantigen toxin DNA fragment), a host
XX cell transformed with the recombinant DNA construct, producing altered
XX superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
XX superantigen toxin peptide, diagnosing superantigen-associated bacterial
XX infection, a vaccine (comprising an altered superantigen toxin for
XX producing antigenic and immunogenic response resulting in the protection
XX of a mammal against superantigen-associated bacterial infection),
XX treating/ameliorating a superantigen-associated bacterial infection,
XX antiserum isolated from individuals immunised with one or more altered
XX TSST-1 superantigen toxin and an antibody which recognises altered TSST-
XX 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
XX SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and
XX SPEb). The superantigen toxin DNA fragment is useful for preparing a
XX composition for treating or preventing bacterial infection. The present
XX sequence represents the S. aureus enterotoxin A, SEA, MHC binding region
XX Sequence 82 AA;
Query Match 32.2%; Score 399; DB 7; Length 82;
Best Local Similarity 86.6%; Pred. No. 4.3e-32;
Matches 71; Conservative 4; Mismatches 7; Indels 0; Gaps 0;
QY 43 SDQQLFNTLLFKGFFTHGHPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTPN 102
DB 1 SHDQFLQHTILFKGFFTHGHPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGTPN 60
QY 103 KTACMYGGVTLHDNNRLTEKK 124
DB 61 KTACMYGGVTLHDNNRLTEKK 82
RESULT 58
AAW24299
ID AAW24299 standard; protein; 91 AA.
XX AC AAW24299;
XX DT 14-APR-1998 (first entry)
XX

DE Staphylococcus aureus Gene #5 polypeptide sequence 2.
 XX Staphylococcus aureus WCUI 29; antagonist; antibacterial; immunogen;
 KW vaccine; disease; protection; isolation.
 XX Staphylococcus aureus.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 29
 TT /note= "Unspecified amino acid"
 XX
 FN WO9731114-A2.
 XX
 XX 28-AUG-1997.
 PD
 XX
 XX 25-FEB-1997; 97WO-GB000524.
 PF
 XX
 PR 26-FEB-1996; 96GB-00004045.
 XX
 PA (SMIK) SMITHKLINE BEECHAM PLC.
 XX
 PI Burnham MKR, Hodgson JE;
 XX
 XX WPI; 1997-435166/40.
 DR N-PSDB; AAV01865.
 XX
 XX New Staphylococcus aureus polynucleotide and polypeptide(s) - for
 PT isolating antagonist of the polypeptide(s) useful as anti-bacterials.
 FT
 XX
 PS Claim 11; Page 33; 117pp; English.
 XX
 CC The present sequence represents a novel polypeptide, which is optionally
 CC expressed in NCIMB 40771. The polypeptide, and polynucleotide encoding
 CC it, are derived from Staphylococcus aureus. Cells expressing ligands that
 CC binding the polypeptide can be used to isolated candidate compounds that
 CC bind and inhibit the activity of the polypeptide. Such compounds can be
 CC used as anti-bacterial compounds. The polypeptide may also be used as an
 CC immunogen to vaccinate an animal for protection against Staphylococcus
 CC aureus caused disease
 XX
 SQ Sequence 91 AA;
 Query Match 29.9%; Score 370; DB 2; Length 91;
 Best Local Similarity 76.9%; Pred. No. 4.2e-29;
 Matches 70; Conservative 8; Mismatches 13; Indels 0; Gaps 0;
 Qy 107 MYGGVTLHDNRLTEEEKVQVRLVHSHSSEGSTVSVD 197
 Db 1 MYGGVTLHDNRLTEEEKVQVRLVHSHSSEGSTVSVD 197
 Qy 167 FGLYNSDSFGKVGQVRLVHSHSSEGSTVSVD 197
 Db 61 YNLVNSDVFQKVGQVRLVHSHSSEGSTVSVD 91
 RESULT 59
 ABP58460
 ID ABP58460 standard; protein; 217 AA.
 XX
 AC ABP58460;
 XX
 XX 14-APR-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin H.
 DE
 XX Superantigen; staphylococcal enterotoxin H; antibody; cancer; tumour;
 KW cytostatic; vaccine.
 KW
 XX Staphylococcus sp.
 OS
 XX WO20003002143-A1.
 FN
 XX 09-JAN-2003.
 PD

XX 19-JUN-2002; 2002WO-SE001188.
 PF
 XX 28-JUN-2001; 2001SE-00002327.
 PR
 XX (ACTI-) ACTIVE BIOTECH AB.
 PA
 XX Forsberg G, Erlandsson E, Antonsson P, Walse B;
 PI
 XX WPI; 2003-201467/19.
 DR
 XX Conjugate for therapy, has bacterial superantigen with a region in T-cell
 PT receptor and four regions to determine binding to class II major
 PT histocompatibility complex, antibody to cancer associated cell surface
 PT structure.
 XX
 PS Example 3; Fig 3; 102pp; English.
 XX
 CC The present sequence is the protein sequence of staphylococcal
 CC enterotoxin D (SED). The invention provides novel conjugates (see
 CC ABP58454) for human cancer therapy. These comprise an engineered
 CC bacterial superantigen, such as novel SEA/E-120 (see ABP58455), and an
 CC antibody moiety, such as tumour reactive antibody 574. Bacterial
 CC enterotoxins such as SEA, SEE, SED and SEH were used in the molecular
 CC modelling of the engineered superantigens. The superantigens were
 CC engineered to reduce seroreactivity whilst maintaining biological
 CC activity and production levels. The novel conjugates were designed to
 CC target and destroy cancer cells, including cancer of the lung, breast,
 CC colon, kidney, pancreas, ovary, stomach, cervix and prostate (claimed)
 XX
 SQ Sequence 217 AA;
 Query Match 29.6%; Score 366; DB 6; Length 217;
 Best Local Similarity 37.9%; Pred. No. 3.6e-28;
 Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
 Qy 10 KDLRKKSELQNALSNLRQIYYVNEKAITENKESDDQFLENTLLFKGFTGHPMWYNDLLV 69
 Db 1 EDLHDKSELTDALAN--AVQYNHPFIKENIKSDEISGEKDLIFRN--QGDSG-NDLRV 55
 Qy 70 DLGSKDATNKYGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNRLTEEEKVQVRLV 129
 Db 56 KFATADLAQKFKKNVDIYGASFYKCEKISENISECLYGGTTL-NSEKLAQERVIGANV 114
 Qy 130 WIDKQTTVPIDKVTKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQVRLVHSHS 189
 Db 115 WVDGIQKETEL--IRTKKNVTQLQELDIKIRKILSDKVIYKDS---EISKGLIEFDMK 169
 Qy 190 EGSTVSVDLFDQAQGYPTDLRLIYRDNKTINSENL-HIDLXYLT 232
 Db 170 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSKDDSHIDVNLVT 213
 RESULT 60
 ADF89833
 ID ADF89833 standard; protein; 217 AA.
 XX
 AC ADF89833;
 XX
 XX 26-FEB-2004 (first entry)
 DT
 XX Staphylococcal enterotoxin H (SEH) superantigen.
 DE
 XX Superantigen; SAg; Staphylococcal enterotoxin; SE; SEH; cytostatic;
 KW gene therapy; cancer.
 KW
 XX Staphylococcus sp.
 OS
 XX WO2003094846-A2.
 FN
 XX 20-NOV-2003.
 PD
 XX 08-MAY-2003; 2003WO-US014381.
 PF

```

XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0408750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 10; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin A, Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin H (SEH) superantigen.
XX SQ Sequence 217 AA;

Query Match 29.6%; Score 366; DB 8; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.6e-28;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELSORALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLAV 69
DB 1 EDLHDKSELTDALAN--AYGQYNHPFKENTKSDISEGKOLIFRN--QGDSG-NDLRV 55
QY 70 DLGSKDATNKKYGGKVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEEEKVPINL 129
DB 56 KFATADLAQKPKRNVDIYGASFYKCEKISENISECLGGTTL-NSEKLAQERVIGANV 114
QY 130 WIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFGGKQVQRLIVFHS 189
DB 115 WVDGIQKETEL--IRTNKKNVTQLQELDKIRKILSDKIKYKDS---BISKGLIEFDMK 169
QY 190 EGSSTVSYDLFDAGQGVPTDLLRIYRNKNTINSENH--HIDLILYT 232
DB 170 TPRDYSDIYDLKGENDYEDIKYEDNKTLKSDDISHIDVNLVT 213

RESULT 61
ADF89834
ID ADF89834 standard; protein; 242 AA.
XX AC ADF89834;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin I (SEI) superantigen.
XX KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEI; cytostatic;
XX KW gene therapy; cancer.
XX OS Staphylococcus sp.
XX PN W02003094846-A2.

```

```

XX PD 20-NOV-2003.
XX PF 08-MAY-2003; 2003WO-US014381.
XX PR 08-MAY-2002; 2002US-0378988P.
XX PR 15-JUN-2002; 2002US-0389366P.
XX PR 28-AUG-2002; 2002US-0406697P.
XX PR 29-AUG-2002; 2002US-0408750P.
XX PR 01-OCT-2002; 2002US-0415310P.
XX PR 02-OCT-2002; 2002US-0415400P.
XX PR 09-JAN-2003; 2003US-0438686P.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX DR WPI; 2004-011997/01.
XX PT Treating a subject with cancer or malignant diseases comprises
XX PT intratumoral, intrathecal or intracavitary administration of an amount of
XX PT a superantigen composition to the subject.
XX PS Disclosure; SEQ ID NO 11; 91pp; English.
XX CC The invention relates to treating a subject with cancer. The method
XX CC involves administering an amount of a superantigen (SAG) composition
XX CC comprising a molecule selected from: a native SAG protein; its
XX CC biologically active fragment or a biologically active homologue or a
XX CC biologically active fusion protein comprising the SAG or its fragment or
XX CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
XX CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
XX CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAG and
XX CC Clostridium perfringens exotoxin. The method is useful in treating cancer
XX CC or malignant diseases such as malignant pleural effusion, ascites,
XX CC pericardial effusion or meningeal carcinomatosis. The present sequence
XX CC represents a Staphylococcal enterotoxin I (SEI) superantigen.
XX SQ Sequence 242 AA;

Query Match 27.4%; Score 339.5; DB 8; Length 242;
Best Local Similarity 35.6%; Pred. No. 2e-25;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIY----YNEKAITENKESDDQFLENTLLFKGFTGHPWYNDLVLGSKDATN 78
DB 30 VGNLNFYTKHDYIDLKGVTDKNLPIANQLE-----PSTG---TNDLISESNWDEIS 79
QY 79 KYKGGKVDLYGAYGYQCAGGTPNKTACMYGVTLDHNNRLTEEEKVPINLMDGKQTTV 138
DB 80 KFKGKKLDIFGIDYNGPC-----KSKYMYGGATL--SGQYLNSARKIPINLWVNGHKTI 132
QY 139 PIDKVTSSKEVTVQELDLQARHYLHGKFLYNSDSFG--GK-----VQRLIVF 186
DB 133 STDKIATNKKLVTAQEIIDLKRLRYLQEEYNIYGHNTGKGYKSKFYSGFNCKVLV 192
QY 187 HSSEGSTVSYDLFDAGQGVPTDLLRIYRNKNTINSENHIDL 228
DB 193 HLNNEKSFSDLYFTYTGDLGFLVPSFLKIYEDNKIIESEKPHLDV 234

RESULT 62
ADF89837
ID ADF89837 standard; protein; 240 AA.
XX AC ADF89837;
XX DT 26-FEB-2004 (first entry)
XX DE Staphylococcal enterotoxin L (SEL) superantigen.
XX KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEL; cytostatic;
XX KW gene therapy; cancer.

```


RESULT 64

ADF89838
ID ADF89838 standard: protein: 239 AA.

AC ADF89838;

DT 26-FEB-2004 (first entry)

DE Staphylococcal enterotoxin M (SEM) superantigen.

Superantigen; SAG; Staphylococcal enterotoxin; SE; SEM; cytostatic; gene therapy; cancer.

Staphylococcus sp.

PN WO2003094846-A2.

PD 20-NOV-2003.

08-MAY-2003; 2003WO-US014381.

PR 08-MAY-2002: 2002US-0378988P.

28-AUG-2002: 2002US-0406697P.

PR 01-OCT-2002: 2002US-0415310P.

PR 09-JAN-2003; 2003US-0438686P.

PA (TERM/) TERMAN D S.

PI Terman DS:

XX
DR WPI: 2004-011997/01.

XX PT Treating a subject

[illegible]

XX
PC
Disclosure: See TD N

XX
CC
the invention related to treating a subject with cancer. The method

CC involves administering an amount of a substance containing a molecule selected from: a D

biologically active fragment or a biologically active homologue or a biologically active fusion protein comprising the SAg or its fragment or biologically active fusion protein comprising the SAg or its fragment or homologue fused to a fusion partner polypeptide or peptide. The SAg is selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic exotoxin, *Y. pseudotuberculosis* SAg, Mycoplasma arthritides SAg and Clostridium perfringens exotoxin. The method is useful in treating cancer or malignant diseases such as malignant pleural effusion, ascites, pericardial effusion or meningeal carcinomatosis. The present sequence represents a Staphylococcal enterotoxin M (SEM) superantigen.

Sequence 239 AA:

Query Match 25.8%; Score 320; DB 8; Length 239;

Best Local Similarity	33.0%	Pred. No. 1.8e-23;
Matches	72; Conservative	40; Mismatches 78;
		Indels 28; Gaps 6;

25 NLRQIYYNEKAITENK--ESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATNKYKG 82 QY

Db 28 NLRN--YGYSPIDHQSIENPNHLSQLVFS-----MDNSTVTAEFKQVDVKKPKN 79

QY 83 KKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEEEKVPINLWIDGKQTTVPIDK 142

Db 80 HAVDVYGLSYSGYCL-----KNKIYGGVTL-AGDYLEKSRRIPLNLWNGEHQTITSDK 133

143 VKTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGGKVQRGGLIVFHSSE 190

Db

QY 136 TTVPIDKVKTSKEVTVOELDLQARHYLHGKFLYN-----SDSFGGKVQRGL 183
Db 130 NTISTDKVSTOKVEVTAQEIIDLKRLQNEVNYGFNKKKGQVGYGKSFNSFNKGK 189
QY 184 IVFHSSEGSTVSVDLFDQAQGVPTDLLRIYRDNKTINSENHLIDL 228
Db 190 ITFHLNNEPSTYDLFTYGTGAESFLTYINDNKTIDAENPHLDV 234

RESULT 66
ADF89836
ID ADF89836 standard; protein; 242 AA.
XX
AC ADF89836;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin K (SEK) superantigen.
XX
KW Superantigen; SAg; Staphylococcal enterotoxin; SE; SEK; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US014381.
XX
PR 08-MAY-2002; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
PA (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 2004-011997/01.
XX
DR
DR
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 13; 91pp; English.
XX
CC The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAg, Mycoplasma arthritides SAg and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin K (SEK) superantigen.
XX
SQ Sequence 242 AA;

Query Match 25.0%; Score 310; DB 8; Length 242;
Best Local Similarity 33.2%; Pred. NO. 1.8e-22;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY-----YNEKAITENKESDDQFLENTLLFKGFFTGHPYNDLLVDLGSKDYN 78
Db 29 IDNLRNFYTKKDFINLKDVKON----DTPIANQLQF-----SNESY-DLISESKDFNKFS 78

QY 79 KYGKGVLDLYGAYTYCYOCAGCTPNKTACMYGGVTLHDNNRLTEBKVPINLWIDGKQTTV 138
Db 79 NFKGKLDVFGISYNGQC-----NTKYIYGITA-TNEYLDKPRNIPINIWINGHXTI 131
QY 139 PIDKVKTSKEVTVOELDLQARHYLHGKFLY-----NSDSFGK-----VORGLVVF 186
Db 132 STNKVSTNKKFVTAQEIIDLKRLRYLQBEYNTYGHNGTKKGEEYGHKSKFYSGFNIGKVTF 191
QY 187 HSSEGSTVSVDLFDQAQGVPTDLLRIYRDNKTINSENHLIDL 228
Db 192 HLNNDTFSYDLFTYGTGDLGPKSLKIYEDNKTVESEKFHLDV 234

RESULT 67
ABU79069
ID ABU79069 standard; protein; 266 AA.
XX
AC ABU79069;
XX
DT 18-JUN-2003 (first entry)
XX
DE S. aureus SEB (staphylococcus enterotoxin B) protein.
XX
KW Superantigen; SAg; staphylococcal enterotoxin; tumour; cancer; apoptosis;
KW gene therapy; mammalian cell receptor; tumour associated lipid; anergy;
KW T cell; antigen presenting cell; tumouricidal immunocyte; cytostatic;
KW APC; antitumour.
XX
OS Staphylococcus aureus.
XX
PN US2002177551-A1.
XX
PD 28-NOV-2002.
XX
PF 30-MAY-2001; 2001US-00870759.
XX
PR 31-MAY-2000; 2000US-0208128P.
XX
XX (TERM/) TERMAN D S.
XX
XX Terman DS;
XX
XX WPI; 2003-361759/34.
XX N-PSDB; ACA64695.
XX
PT A mammalian cell receptor, useful in the treatment of cancer by binding
PT to tumour associated lipids where the binding induces anergy or apoptosis
PT in T cells and antigen presenting cells.
XX
PS Disclosure; Page; 167pp; English.

The invention relates to a mammalian cell receptor, useful in the treatment of cancer, which binds to tumour associated lipids and induces anergy or apoptosis in the T cells and antigen presenting cells (APCs). Also included are a mammalian cell useful in the treatment of cancer where the receptor which binds tumour associated lipids and induces cellular inactivation or death is deleted or functionally deactivated, producing (M1) a tumouricidal immunocyte population in vivo in a mammal (by allowing tumour associated lipids to contact immunocytes in which receptors for immunosuppressive fatty acids, ceramides, glycolipids, sphingolipids, glycosphingolipids, phosphosphingolipids, gangliosides, sialylated glycans, lipopeptides and proteoglycolipids are inactivated or deleted); a construct useful in the treatment of cancer comprising a superantigen (SAG) nucleotide inserted into a virus, a mammalian T cell useful in the treatment of cancer (where an adaptor protein which inhibits T cell activation by tumour associated antigens is deleted or functionally deactivated), a composition useful in the treatment of cancer (comprising a lipid raft conjugated to a superantigen), producing (M2) a tumouricidal immunocyte population ex vivo in a mammal (by allowing tumour associated lipids to contact immunocytes, in which receptors for the lipids are inactivated or deleted to produce a tumouricidal immunocyte population, and administering the tumouricidally activated immunocytes to the host), producing (M3) a tumouricidal APC

population ex vivo in a mammal (by allowing a tumour associated lipid to contact APCs, in which receptors for the tumour associated lipids are inactivated or deleted to produce a tumouricidally activated population, and administering APCs to the host), producing a tumouricidal T cell population ex vivo in a mammal) by allowing a tumour associated lipids to contact T cells, in which adaptor proteins, which inhibit T cell activation by tumour associated antigens, are deleted or functionally deactivated to produce a tumouricidally activated T cells, and administering the tumouricidally activated T cells to the host, or allowing a superantigen-lipid raft to contact T cells ex vivo, and administering the tumouricidally activated T cells to the host). treating (M5) cancer in a mammal (by administering a lipid binding molecule which binds immunosuppressive tumour associated lipids in vivo), producing (M6) a tumouricidal T cell population in vivo in a mammal (by allowing a tumour associated antigen to contact immunocytes in which adaptor proteins which inhibit T cell activation by tumour associated antigens are deleted or functionally deactivated) and producing (M7) a tumouricidal T cell population ex vivo in a mammal comprising allowing a superantigen-lipid raft conjugate to contact immunocytes in vivo. The receptors, methods and compositions are useful for treating cancers and tumours. Bacterial superantigens are co-administered or administered as fusion constructs with anti-tumour proteins or motifs. The present sequence represents a bacterial superantigen protein (e.g. a staphylococcal enterotoxin). Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format from the US patent office website at "seqdata.uspto.gov/sequence.html?DocID=20020177551"

Sequence 266 AA;

Query Match 24.3%; Score 300.5; DB 6; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.9e-21;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 27 AESQDPKPKDELHKSKF-TGLMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGYNDNVRVEFRKDLADKYKVDVFGANYYYQCYFSKKTNDINSHQDTRKTCMYGG 144
QY 111 VTLDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGY 170
DB 145 VTEHNGQLDKYRSITVRVEDCK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKLY 202
QY 171 NSDSFGKVGQRLIVFHSSEGSTVSVDLFDACQOYPD--TLRIYRDNKNTINSENHLIDL 228
DB 203 EFNN--SPYETGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNMVDKVKIEV 259
QY 229 YLYT 232
DB 260 YLTT 263

RESULT 68

ABG75015
ID ABG75015 standard; protein; 266 AA.

AC ABG75015;

XX 12-FEB-2004 (first entry)

DE S aureus enterotoxin B protein.

XX Enterotoxin B; SEB; immunomodulatory; IgE antibody; atopic eczema;
KW lupus erythematosus; Crohn's disease; multiple sclerosis; psoriasis;
KW rheumatoid arthritis; immunoglobulin E; dermatological; antiasthmatic;
KW allergic; ophthalmological; antipsoriatic; antirheumatic;
KW antiarthritic; neuroprotective; immunosuppressive; antiinflammatory;
KW vasotrophic; antidiabetic; thyromimetic; antibacterial; gynaecological;
KW cytosstatic.

OS Staphylococcus aureus.
XX Key Location/Qualifiers
FH Peptide 1..27
FT /label= signal_peptide
FT Protein 28..266
FT /label= mature_protein
XX WO2003068812-A2.
PN 21-AUG-2003.
XX 14-FEB-2003; 2003WO-EP001511.
PF 15-FEB-2002; 2002DE-01007734.
PR 04-SEP-2002; 2002DE-01040866.
XX (AGEL-) AGELAB PHARMA GMBH.
PA Neuber K;
XX WPI; 2003-646480/61;
DR N-PSDB; ACH00502.
XX New polypeptide that binds immunoglobulin E and alters cytokine synthesis, useful for treating e.g. atopic eczema, asthma or allergy, also its encoding nucleic acid.
PS Disclosure; Page 43-44; 46pp; German.
XX The present invention relates to novel peptides derived from Staphylococcus aureus enterotoxin B (SEB) protein. These peptides are capable of binding to immunoglobulin (Ig) E antibodies. However, unlike SEB, they do not induce proliferation of T cells. The peptides are useful as immunomodulators and inhibitors of cytokine production in T cells, particularly for treatment of atopic eczema, bronchial asthma, allergic rhinoconjunctivitis, psoriasis, rheumatoid arthritis and multiple sclerosis and for inducing or strengthening the Th1/Th2 immune responses specifically for treating psoriasis, autoimmune uveitis, allergic contact eczema, Behcet's syndrome, diabetes mellitus, Hashimoto's thyroiditis, infection by Helicobacter pylori, lupus erythematosus, Crohn's disease, multiple sclerosis, organ transplant rejection, rheumatoid arthritis and spontaneous recurrent abortion. They can also be used, in vitro, for inhibiting IFN-gamma production and for modulating spontaneous or stimulated cytokine production in Th1/Th2 cells. The present sequence is the SEB protein as used in the exemplification of the invention

Sequence 266 AA;

Query Match 24.3%; Score 300.5; DB 7; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.9e-21;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;
QY 1 SEKSEINEKDLRKKSSELQNALSNLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
DB 27 AESQDPKPKDELHKSKF-TGLMENMKVLYDDNHVSAL-NVKSIDQFLYFDLIYSIKDTK 84
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGG 110
DB 85 LGYNDNVRVEFRKDLADKYKVDVFGANYYYQCYFSKKTNDINSHQDTRKTCMYGG 144
QY 111 VTLDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDQARHYLHGKFGY 170
DB 145 VTEHNGQLDKYRSITVRVEDCK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKLY 202
QY 171 NSDSFGKVGQRLIVFHSSEGSTVSVDLFDACQOYPD--TLRIYRDNKNTINSENHLIDL 228
DB 203 EFNN--SPYETGYIKFTIENENS-FWYDMPAPGDKFDQSKYLMYNDNKNMVDKVKIEV 259
QY 229 YLYT 232
DB 260 YLTT 263

```
RESULT 69
ADF43290
ID  ADF43290 standard; protein; 266 AA.
XX
AC  ADF43290;
XX
DT  12-FEB-2004 (first entry)
XX
DE  Staphylococcal enterotoxin B polypeptide seq id 10.
XX
KW  receptor; lipid-based tumour associated antigen; cytostatic;
KW  antimicrobial; gene therapy; neoplastic disease; tumour; cancer;
KW  infectious disease; Staphylococcal enterotoxin B; SEB; enterotoxin B.
XX
OS  Staphylococcus.
XX
FN  US2003157113-A1.
XX
PD  21-AUG-2003..
XX
PF  28-DEC-2000; 2000US-00751708.
XX
PR  28-DEC-1999; 99US-0173371P.
XX
PA  (TERM/) Terman D S.
XX
PI  Terman DS;
XX
DR  WPI; 2003-787326/74.
XX
PT  New receptor in a mammalian cell that inhibits regular activation by
PT  receptors specific for lipid-based tumor associated antigens, useful for
PT  treating a neoplastic disease or tumor, and infectious diseases.
XX
PS  Example 3; SEQ ID NO 10; 151pp; English.
XX
CC  The invention describes a receptor in a mammalian cell that inhibits
CC  regular activation by receptors specific for lipid-based tumour
CC  associated antigen. The receptor has cytostatic and antimicrobial
CC  properties and is suitable for use in gene therapy. The receptors,
CC  methods and compositions are useful for treating a neoplastic disease or
CC  tumour (cancer), and infectious diseases. This is the amino acid sequence
CC  of an enterotoxin superantigen polypeptide the DNA encoding which can be
CC  transfected in to a cell alone or with DNA encoding a cell surface moiety
CC  to generate antitumour immunity.
XX
SQ  Sequence 266 AA;

Query Match      24.3%; Score 300.5; DB 7; Length 266;
Best Local Similarity 33.6%; Pred. No. 1.9e-21;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;

Qy  1 SEKSEINEKDLRKSEQLRNALSNLROIYYNKAITENKESDDQFLNTLLFKGFTG 60
Db  27 AESQDPDPKDELHKSKE-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTK 84
Qy  61 HPWNDDLLVDLGSKDATHKYKKVDLYGAYGYQC-----AGGTNKTACMYGG 110
Db  85 LGNYDNVRVFPKNDLADKYDKYDVFVGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144
Qy  111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLOARHVLHGKFGLY 170
Db  145 VTEHNGQLDKRSITRVFPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHVLVKNKKLY 202
Qy  171 NSDSFGGKQVRGLIVFHSSEGSTVSYDLFDAQQGYD--TLLRIYRDNKNTINSENHLIDL 228
Db  203 EFNN--SPYENGYIKFIENENS-FWYDNWMPAPGDKFDQSKYLMYNDNKNWDSKDVKIEV 259
Qy  229 YLYT 232
Db  260 YLTT 263
```

```
RESULT 70
AAW06737
ID  AAW06737 standard; protein; 255 AA.
XX
AC  AAW06737;
XX
DT  08-MAR-1997 (first entry)
XX
DE  Staphylococcus enterotoxin B.
XX
KW  Enterotoxin B; superantigen; antigen; cytokine; chemokine; T cell;
KW  lymphocyte; monocyte; natural killer cell; gene therapy; cancer; vaccine;
KW  adjuvant.
XX
OS  Staphylococcus sp.
XX
FH  Key Location/Qualifiers
FT  Peptide 1..15
FT  /label= Sig_peptide
XX
PN  WO9636366-A1.
XX
PD  21-NOV-1996.
XX
PF  20-MAY-1996; 96WO-US007432.
XX
PR  18-MAY-1995; 95US-00446918.
PR  29-DEC-1995; 95US-00580806.
XX
PA  (NAJE-) NAT JEWISH CENT IMMUNOLOGY & RESPIRATORY.
XX
PI  Dow SW, Elmslie RE, Potter TA;
XX
DR  WPI; 1997-011857/01.
DR  N-PSDB; AAT45698.
XX
XX  Recombinant molecule encoding superantigen and opt. cytokine or
XX  chemokine - controls activity of effector cells (T cells, monocytes,
XX  natural killer cells), used for gene therapy of cancer.
XX
PS  Example 1; Page 96-97; 131pp; English.
XX
CC  A cDNA clone (AAT45698) codes for staphylococcal enterotoxin B (AAW06737)
CC  superantigen. Nucleic acids encoding superantigens (see also AAW06738-
CC  39), esp. truncated forms of the superantigen lacking the leader peptide,
CC  can be utilised in the gene therapy of cancer, infectious diseases and
CC  immunological disorders. The nucleic acid, optionally in combination with
CC  cytokine or chemokine nucleic acids, is delivered to an animal using e.g.
CC  liposomes. It acts by controlling the activity of effector cells, such as
CC  T-cells, macrophages, monocytes and/or natural killer cells. Localised
CC  prodn. of an effective but non-toxic amount of encoded proteins allows
CC  safe treatment of the animal
XX
SQ  Sequence 255 AA;

Query Match      24.2%; Score 300; DB 2; Length 255;
Best Local Similarity 34.0%; Pred. No. 2e-21;
Matches 83; Conservative 46; Mismatches 97; Indels 18; Gaps 7;

Qy  1 SEKSEINEKDLRKSEQLRNALSNLROIYYNKAITENKESDDQFLNTLLFKGFTG 60
Db  15 SMESQDPDPKDELHKSKEFTGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTK 73
Qy  61 HPWNDDLLVDLGSKDATHKYKKVDLYGAYGYQC-----AGGTNKTACMYGG 110
Db  74 LGNYDNVRVFPKNDLADKYDKYDVFVGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 133
Qy  111 VTLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVQELDLOARHVLHGKFGLY 170
Db  134 VTEHNGQLDKRSITRVFPEDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHVLVKNKKLY 191
Qy  171 NSDSFGGKQVRGLIVFHSSEGSTVSYDLFDAQQGYD--TLLRIYRDNKNTINSENHLIDL 228
```

Db 192 BFNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNRKQVDSKDVKIEV 248
Qy 229 YLYT 232
Db 249 YLYT 252

RESULT 71
ADF89825
ID ADF89825 standard; protein; 238 AA.
XX
AC ADF89825;
XX
DT 26-FEB-2004 (first entry)
XX
DE Staphylococcal enterotoxin B (SEB) superantigen.
XX
KW Superantigen; SAG; Staphylococcal enterotoxin; SE; SEB; cytostatic;
KW gene therapy; cancer.
XX
OS Staphylococcus sp.
XX
PN WO2003094846-A2.
XX
PD 20-NOV-2003.
XX
PF 08-MAY-2003; 2003WO-US014381.
XX
PR 08-MAY-2003; 2002US-0378988P.
PR 15-JUN-2002; 2002US-0389366P.
PR 28-AUG-2002; 2002US-0406697P.
PR 29-AUG-2002; 2002US-0406750P.
PR 01-OCT-2002; 2002US-0415310P.
PR 02-OCT-2002; 2002US-0415400P.
PR 09-JAN-2003; 2003US-0438686P.
XX
PA (TERM/) TERMAN D S.
XX
PI Terman DS;
XX
WPI; 2004-011997/01.
XX
DR
PT Treating a subject with cancer or malignant diseases comprises
PT intratumoral, intrathecal or intracavitary administration of an amount of
PT a superantigen composition to the subject.
XX
PS Disclosure; SEQ ID NO 2; 91pp; English.
XX
CC The invention relates to treating a subject with cancer. The method
CC involves administering an amount of a superantigen (SAG) composition
CC comprising a molecule selected from: a native SAG protein; its
CC biologically active fragment or a biologically active homologue or a
CC biologically active fusion protein comprising the SAG or its fragment or
CC homologue fused to a fusion partner polypeptide or peptide. The SAG is
CC selected from Staphylococcal enterotoxin, a Streptococcal pyrogenic
CC exotoxin, Y. pseudotuberculosis SAG, Mycoplasma arthritidis SAG and
CC Clostridium perfringens exotoxin. The method is useful in treating cancer
CC or malignant diseases such as malignant pleural effusion, ascites,
CC pericardial effusion or meningeal carcinomatosis. The present sequence
CC represents a Staphylococcal enterotoxin B (SEB) superantigen.
XX
SQ Sequence 238 AA;

Query Match 24.2%; Score 299.5; DB 8; Length 238;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPKDELHKSSRP-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
Qy 62 PWTNDLLVLDGSDATNKKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGGV 111

Db 59 GYDNVRVEFFKNLADKYDKYVDVFGANTYYQCYFSKTKNDINSHQTDKRKTCMYGV 118
Qy 112 TLHNNRLTEERKVPINLWIDGKQTTVPIDIKVTKTSKKEVTVQELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVPEDGK-NLLSFD-VQTNKKVTAQELDYLTRHYLVKNKLYE 176
Qy 172 SDSFGKVQRLIVPHSSEGSTSVYDLFPAQGOYPD--TLRIYRDNKTINSENHIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMYNDNRKQVDSKDVKIEV 233
Qy 230 LYT 232
Db 234 LYT 236

RESULT 72
AAW64647
ID AAW64647 standard; peptide; 239 AA.
XX
AC AAW64647;
XX
DT 23-OCT-1998 (first entry)
XX
DE Synthetic SEB protein fragment.
XX
KW Enterotoxin B; SEB; pyrogenic exotoxin; PET; protective immunity;
KW toxic shock; toxin-mediated activation; T-cell; antagonist; inhibitor;
KW therapeutic; vaccine; food poisoning.
XX
OS Synthetic.
OS Staphylococcus aureus.
XX
PN WO9829444-A1.
XX
PD 09-JUL-1998.
XX
PF 30-DEC-1997; 97WO-IL000438.
XX
PR 30-DEC-1996; 96IL-00119938.
XX
PA (YISS) YISSUM RES & DEV CO.
XX
PI Kaempfer R, Arad G;
XX
DR WPI; 1998-388042/33.
XX
PT New peptide(s) derived from pyrogenic exotoxin - useful for, e.g.
PT antagonising toxin-mediated activation of T cells and prevention or
PT treatment of toxic shock caused by exotoxin(s).
XX
PS Example 8; Page 41; 68pp; English.
XX
CC AAW64636-W64657 are peptides homologous to the amino acid sequence of a
CC fragment of a pyrogenic exotoxin (PET), and derivatives of the peptide
CC capable of eliciting protective immunity against toxic shock induced by
CC PET or by a mixture of PETs. Such peptides are also capable of
CC antagonising toxin-mediated activation of T-cells, inhibiting expression
CC of pyrogenic toxin (PT)-induced mRNA encoded by IL-2, IFN-gamma or TNF-
CC beta genes. The peptides may be used to prepare therapeutics or vaccines
CC for the treatment of prophylaxis of toxin-mediated activation of T cells
CC and eliciting protective immunity against toxic shock induced by PETs.
CC They can also be used for the treatment of harmful effects (especially
CC food poisoning) and toxic shock caused by PET. Antiserum to the peptides
CC can also be used for alleviating toxic shock induced by PET
XX
SQ Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 2; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61

Db 1 ESQPDPKDELHKSSKF-TGLMENNKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKOTKL 58
Qy 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKATCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHETDKRKTCTMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHLYLVNKKLYE 176
Qy 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENLIHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 73
AAB67341
ID AAB67341 standard; peptide; 239 AA.
XX AC AAB67341;
XX DT 23-APR-2001 (first entry)
XX DE Staphylococcus aureus enterotoxin B protein.
XX XX Tumour; cancer; immune; enterotoxin.
XX OS Staphylococcus aureus.
XX PN USG180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX XX 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX PA (TERM/) TERMAN D S.
XX PI Terman DS;
XX XX WPI; 2001-158657/16.
XX DR
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX XX The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
XX XX Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 4; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;

Qy 2 EKSEINEKDLRKSELRNALSRLQIYYNYNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQPDPKDELHKSSKF-TGLMENNKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKOTKL 58
Qy 62 PWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQC-----AGTTPNKATCMYGGV 111
Db 59 GNYDNVRVEFNKDLADKYDKYVDVFGANYYYQCYFSKKTNDINSHQTDKRKTCTMYGGV 118
Qy 112 TLHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTVOELDLQARHYLHGKFGLYN 171
Db 119 TEHNGNQLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVTQAQELDYLTRHLYLVNKKLYE 176
Qy 172 SDSFGGKVQGLIVFHSSEGSTVSVDLFDAGQGYPD--TLRIYRDNKNTINSENLIHDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFDQSKYLMYNDNKNVDSKDVKIEVY 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 74
ABG75016
ID ABG75016 standard; protein; 239 AA.
XX AC ABG75016;
XX XX 12-FEB-2004 (first entry)
XX DE Unidentified Staphylococcus aureus protein.
XX KW Enterotoxin B; SEB; immunomodulatory; IgE antibody; atopic eczema;
XX KW lupus erythematosus; Crohn's disease; multiple sclerosis; psoriasis;
XX KW rheumatoid arthritis; immunoglobulin E; dermatological; antiasthmatic;
XX KW antiallergic; ophthalmological; antipsoriatic; antineumatic;
XX KW antiarthritic; neuroprotective; immunosuppressive; antiinflammatory;
XX KW vasotropic; antidiabetic; thyromimetic; antibacterial; gynaecological;
XX KW cytostatic.
XX OS Staphylococcus aureus.
XX XX WO2003068812-A2.
XX PN 21-AUG-2003.
XX PD 14-FEB-2003; 2003WO-EP001511.
XX PF 15-FEB-2002; 2002DE-01007734.
XX PR 04-SEP-2002; 2002DE-01040866.
XX XX (AGEL-) AGELAB PHARMA GMBH.
XX PI Neuber K;
XX XX WPI; 2003-646480/61.
XX DR
XX PT New polypeptide that binds immunoglobulin E and alters cytokine
XX PT synthesis, useful for treating e.g. atopic eczema, asthma or allergy,
XX PT also its encoding nucleic acid.
XX PS Disclosure; Page 45-46; 46pp; German.
XX XX The present invention relates to novel peptides derived from
XX CC Staphylococcus aureus enterotoxin B (SEB) protein. These peptides are
XX CC capable of binding to immunoglobulin (Ig) E antibodies. However, unlike
XX CC SEB, they do not induce proliferation of T cells. The peptides are useful
XX CC as immunomodulators and inhibitors of cytokine production in T cells,
XX CC particularly for treatment of atopic eczema, bronchial asthma, allergic
XX CC rhinoconjunctivitis, psoriasis, rheumatoid arthritis and multiple
XX CC sclerosis and for inducing or strengthening the Th1/Th2 immune responses,
XX CC specifically for treating psoriasis, autoimmune uveitis, allergic contact
XX CC eczema, Behcet's syndrome, diabetes mellitus, Hashimoto's thyroiditis,

CC infection by Helicobacter pylori, lupus erythematosus, Crohn's disease,
CC multiple sclerosis, organ transplant rejection, rheumatoid arthritis and
CC spontaneous, recurrent abortion. They can also be used, in vitro, for
CC inhibiting IFNgamma production and for modulating spontaneous or
CC stimulated cytokine production in Th1/Th2 cells. Note: No further
CC information about this sequence is given in the specification
XX
SQ Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 7; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELRNALSRLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
QY 112 TLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFEDEK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNKLYE 176
QY 172 SDSFGKVGQRLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMVDSKDKVIEY 233
QY 230 LYT 232
Db 234 LIT 236

RESULT 75
ADL14247
ID ADL14247 standard; protein; 239 AA.

XX ADL14247;
XX 20-MAY-2004 (first entry)
XX Wild type Staphylococcus aureus enterotoxin B protein.
XX
XX staphylococcal enterotoxin B; SEB; immunogenicity;
XX T-cell peptide epitope; immune response.
XX Staphylococcus aureus.
XX WO2004018684-A2.
XX
XX 04-MAR-2004.
XX
XX 18-AUG-2003; 2003WO-EP009116.
XX
XX 21-AUG-2002; 2002EP-00018229.
XX (MERE) MERCK PATENT GMBH.
XX Carr FJ, Baker M, Carter G;
XX WPI; 2004-226855/21.
XX

XX New modified molecule having the biological activity of staphylococcal
XX enterotoxin B (SEB), useful as determinants on SEB able to evoke an
XX immune response.
XX
XX Disclosure; Page 4; 38pp; English.
XX
XX This invention relates to novel modified proteins that exhibit the
XX biological activity of Staphylococcal enterotoxin B (SEB) with reduced
XX immunogenicity compared to wild type proteins having the same biological
XX activity. Specifically, it refers to the identification of T-cell peptide

CC epitopes derived from SEB that can be modified in order to create
CC variants that are non-immunogenic. The present invention describes
CC designing SEB analogues containing amino acid substitutions in the most
CC immunogenic regions. Accordingly, the resulting modified molecules are
CC useful as determinants on SEB able to evoke an immune response. This
CC polypeptide sequence is the Staphylococcus aureus enterotoxin B protein
CC of the invention.
XX
SQ Sequence 239 AA;

Query Match 24.2%; Score 299.5; DB 8; Length 239;
Best Local Similarity 33.7%; Pred. No. 2.1e-21;
Matches 82; Conservative 46; Mismatches 96; Indels 19; Gaps 8;
QY 2 EKSEINEKDLRKSELRNALSRLRQIYYNNEKAITENKESDDQFLENTLLFKGFFTGH 61
Db 1 ESQDPKPELHKSSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTCMYGGV 111
Db 59 GNYDNVRVEFKNDLADKYKDYVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGGV 118
QY 112 TLHDNNRLTEEEKVPINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFLYN 171
Db 119 TEHNGNQLDKYRSITVRVFEDEK-NLLSFD-VQTNKKKVTAGELDLTRHYLVKNKLYE 176
QY 172 SDSFGKVGQRLIVFHSSEGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDMMPAGDKFDQSKYLMYNDNMVDSKDKVIEY 233
QY 230 LYT 232
Db 234 LIT 236

RESULT 76
AAW12153
ID AAW12153 standard; protein; 251 AA.

XX AAW12153;
XX 04-NOV-1997 (first entry)
XX Streptococcus pyogenes Streptococcal toxin A mutant Cys90Ser.
XX
XX Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
XX protection; treatment; cancer; neutralising antibody;
XX streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
XX hypotension; group A streptococcal infection; myositis; fascitis;
XX liver damage; T cell; lymphoma; ovarian; uterine.
XX Streptococcus pyogenes.
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Peptide 1..30
XX /label= sig_peptide
XX Peptide 31..251
XX /label= mat_peptide
XX Misc-difference 120
XX /note= "wild type Cys replaced by Ser"
XX
XX WO9640930-A1.
XX
XX 19-DEC-1996.
XX
XX 07-JUN-1996; 96WO-US010252.
XX
XX 07-JUN-1995; 95US-00480261.
XX
XX (MINU) UNIV MINNESOTA.
XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

WPI; 1997-099936/09.

Mutant SPE-A toxin with at least one amino acid change is substantially non-lethal - used in vaccine composition for treatment of cancer and streptococcal toxic shock syndrome etc.

Example 4; Page; 102pp; English.

The present sequence is a non-lethal *Streptococcus pyogenes* Streptococcal toxin A (SPE-A) mutant, which can be used to produce vaccines to protect animals against wild type SPE-A and to treat cancer and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes neutralising antibodies (Ab) to be produced, which may be used to ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal infection, myositis, fascitis and liver damage. The neutralising Ab is preferably administered in conjunction with antibiotic therapy. The mutant SPE-A is especially useful for treating T cell lymphomas, and ovarian and uterine cancer. It is thought that mutant SPE-A can be selectively toxic to T cell lymphoma cells. N.B. Sequence not given in the specification, but constructed using the wild type SPE-A sequence given on pages 77-79

Sequence 251 AA;

XX	26-NOV-2001; 2001US-00002784.	
XX		
XX	25-JUN-1997; 97US-00882431.	
PR	01-SEP-1998; 98US-00144776.	
XX		
PA	(ULRI/) ULRICH R G.	
XX		
PI	Ulrich RG;	
XX		
DR	WPI; 2003-492125/46.	
XX		
PT	New superantigen toxin DNA fragment, useful for preparing a composition	
PT	for treating or preventing bacterial infection.	
XX		
XX	Example 3; Page: 68pp; English.	
XX		
CC	The invention relates to an isolated and purified superantigen toxin DNA	
CC	fragment is altered so that binding of the encoded altered toxin to	
CC	either the MHC class II or T cell antigen receptor is altered. Also	
CC	included are a recombinant DNA construct (comprising a vector and an	
CC	isolated and purified altered superantigen toxin DNA fragment), a host	
CC	cell transformed with the recombinant DNA construct, producing altered	
CC	superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)	
CC	superantigen toxin peptide, diagnosing superantigen-associated bacterial	
CC	infection, a vaccine (comprising an altered superantigen toxin for	
CC	producing antigenic and immunogenic response resulting in the protection	
CC	of a mammal against superantigen-associated bacterial infection),	
CC	treating/ameliorating a superantigen-associated bacterial infection, an	
CC	antiseria isolated from individuals immunised with one or more altered	
CC	TSST-1 superantigen toxin and an antibody which recognises altered TSST-	
CC	1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,	
CC	SEB, SEC1) and streptococcal pyrogenic enterotoxin a and b (SPEa and	
CC	SPeB). The superantigen toxin DNA fragment is useful for preparing a	
CC	composition for treating or preventing bacterial infection. The present	
CC	sequence represents the Y94A (with reference to the mature protein	
CC	sequence) mutant of SEB. Note: The present sequence is not shown in the	
CC	specification but was created by the indexer using the wild-type sequence	
CC	and the information in the specification	
XX		
XX	Sequence 266 AA;	
XX		
Query Match	24.0%; Score 297.5; DB 7; Length 266;	
Best Local Similarity	33.2%; Pred. No. 3.8e-21;	
Matches	81; Conservative 44; Mismatches 100; Indels 19; Gaps 7	
QY	1 SEKSEEINEXDLRKKSLQRNALSNLRQIYYNEKAITENKESDDQFLENTLLKGFFTG 60	
Db	27 AESQDPKPELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTRK 84	
QY	61 HPWYNDDLVLGSKDADNATYKKGKVDYLGAYGYQCAGG-----TPNKTACMYGG 110	
Db	85 LGDYDNRVRFKQNLADKYKDKVDVFGANYYQCAFSEKKTNDINSHQTDKRKTCMYGG 144	
QY	111 VTLHDNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLY 170	
Db	145 VTEHNGQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNNKKY 202	
QY	171 NSDSFGKGVORGLTVFHSSEGSTVSYDLFDAQQG--YPDTLRLIYRDNKTINSENHLIDL 228	
Db	203 EFNN--SPYETGYIKFIENENS-FWYDMMPAGDKFAQSKYLMYNDKNWDSKDVKIEV 259	
QY	229 YLYT 232	
Db	260 YLTT 263	
RESULT 78		
AAR13209		
ID	AAR13209 standard; protein; 221 AA.	
XX		
AC	AAR13209;	
XX		

DT 27-AUG-2003 (revised)
 DT 15-OCT-1991 (first entry)
 XX Streptococcal pyrogenic enterotoxin A.
 DE SPE A; cancer treatment; pyrogen; tumouricide; scarlet fever.
 KW Streptococcus sp.
 XX WO9110680-A.
 XX 25-JUL-1991.
 PD 17-JAN-1990; 90US-00466577.
 XX 17-JAN-1990; 90US-00466577.
 PR (TERM/) TERMAN D S.
 XX Terman DS;
 PI WPI; 1991-237984/32.
 DR Treating cancer with enterotoxin from *Staphylococcus aureus* -
 XX administered by IV injection, having same tumoricidal activity as
 CC *Staphylococcal* protein A without potential toxic reactions.
 PT Disclosure; Fig 1; 74pp; English.
 XX SPE A can be used for tumoricidal treatment, esp. with a haemolysin.
 CC Synthetic polypeptides having structural homology to *Streptococcal*
 CC pyrogenic exotoxins are claimed, provided the homology includes
 CC statistically significant sequence homology, alignment of Cysteine
 CC residues and similar hydrophathy profiles. See AAR13203-R13211. (Updated
 CC on 27-AUG-2003 to correct OS field.)
 XX Sequence 221 AA;
 SQ

Query Match 23.9%; Score 296.5; DB 2; Length 221;
 Best Local Similarity 35.6%; Pred. No. 3.7e-21;
 Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;

QY 16 SELQRNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLPKGFPTGHPWINDLLVDLG 72
 Db 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN--VSGPNYDKLKTLEK 63
 QY 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVGTLDHNNRLTEEEKVPINLWI 131
 Db 64 NQEMATLFDKQNDIYGVVEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVKVSI 123
 QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIVFHSSEG 191
 Db 124 DGIQ-SLSFD-IETNKKVMTAQELDYKVRKYLTDNKLTYNGP--SKYETGYIKFIPKPK 179
 QY 192 STVSVYDLFD---AQGYPTDLRLIYRDNKTINSENHLDLYLT 232
 Db 180 ESWFDFLPPEPFTQSKY----LMIYKDNETLDSNTSQIEVILTT 220

RESULT 80
 AAR45017
 ID AAR45017 standard; protein; 221 AA.
 AC AAR45017;
 XX 25-MAR-2003 (revised)
 DT 08-JUN-1994 (first entry)
 XX *Staphylococcal* enterotoxin SPE A.
 DE *Staphylococcal* enterotoxin; SE; cancer; tumoricidal agent;
 KW autoimmune disease; toxicity; Protein A; perfusion system.

OS *Staphylococcus aureus*.
 XX WO9324136-A1.
 PN 09-DEC-1993.
 PD 01-JUN-1993; 93WO-US005213.
 XX 01-JUN-1992; 92US-00891718.
 PR (TERM/) TERMAN D S.
 PA (STON/) STONE J L.
 XX Terman DS, Stone JL;
 PI WPI; 1993-405418/50.
 DR Use of *staphylococcal* enterotoxin(s) and homologues - for treating cancer
 PT in a patient or for the treatment of auto-immune diseases.
 PT Disclosure; Fig 1; 90pp; English.
 XX The sequences given in AAR45011-21 are *Staphylococcal* enterotoxins (SEs)
 CC which may be used in the methods of the invention for treating cancer in
 CC a patient. These SEs, and homologues of them, can be used as tumoricidal
 CC agents for treating cancers and autoimmune disease. They exhibit
 CC tumoricidal activity and toxicity identical to that observed for the
 CC Protein A perfusion system. They may be administered by i.v. injection.
 CC (Updated on 25-MAR-2003 to correct PN field.)
 XX Sequence 221 AA;
 SQ

Query Match 23.9%; Score 296.5; DB 2; Length 221;
 Best Local Similarity 35.6%; Pred. No. 3.7e-21;
 Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;

QY 16 SELQRNAL-SNLRLQIYY-YNEKAIT-ENKESDDQFLENTLLPKGFPTGHPWINDLLVDLG 72
 Db 7 SQLHRSSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHDLIYN--VSGPNYDKLKTLEK 63
 QY 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMGVGTLDHNNRLTEEEKVPINLWI 131
 Db 64 NQEMATLFDKQNDIYGVVEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKIVVKVSI 123
 QY 132 DGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLGYNDSFGGKVQVGLIVFHSSEG 191
 Db 124 DGIQ-SLSFD-IETNKKVMTAQELDYKVRKYLTDNKLTYNGP--SKYETGYIKFIPKPK 179
 QY 192 STVSVYDLFD---AQGYPTDLRLIYRDNKTINSENHLDLYLT 232
 Db 180 ESWFDFLPPEPFTQSKY----LMIYKDNETLDSNTSQIEVILTT 220

RESULT 80
 ABB76240
 ID ABB76240 standard; protein; 221 AA.
 XX ABB76240;
 AC ABB76240;
 XX 09-AUG-2002 (first entry)
 DT *Staphylococcus pyogenes* exotoxin A.
 DE Exotoxin A; SPE A; superantigen; antigen; tumour; cancer; antitumour;
 KW therapy.
 XX *Streptococcus pyogenes*.
 OS US2002051765-A1.
 XX 02-MAY-2002.
 PD 19-DEC-2000; 2000US-00741503.
 PF

XX 03-OCT-1989; 89US-00416530.
PR 17-JAN-1990; 90US-00466577.
PR 17-JAN-1991; 91WO-US000342.
PR 01-JUN-1992; 92US-008931718.
PR 02-MAR-1993; 93US-000251144.
PR 31-JAN-1994; 94US-00189424.
PR 19-JUN-1995; 95US-00491746.
XX (TERM/) Terman D S.
XX Terman DS;
XX WPI; 2002-415198/44.
PT Reagent for treating cancer without the need for e.g. radiotherapy,
PT comprises a specific V beta subset of T cells sensitized to a growing
PT tumor and stimulated with superantigens.
XX
PS Disclosure; Fig 2; 17pp; English.
XX
CC The present sequence is the protein sequence of exotoxin A (SPE A) of
CC Streptococcus pyogenes. Similarity is shown, in several stretches of
CC sequence, between staphylococcal enterotoxins, streptococcal pyrogenic
CC exotoxins and staphylococcal exfoliative toxins (see ABB76234-44). In the
CC present invention, synthetic polypeptides useful in tumour therapy and in
CC blocking or destroying autoreactive T and B lymphocyte populations are
CC characterised by subantigenic structural homology to staphylococcal
CC enterotoxin A and enterotoxin B, and to streptococcal pyrogenic
CC exotoxins, with statistically significant sequence homology and
CC similarity (Z value of Lipman and Pearson algorithm in Monte Carlo
CC analysis exceeding 6) to include alignment of cysteine residues and
CC similar hydrophathy profiles. These superantigens are used to treat solid
CC tumours, including their metastases, without radiation, surgery or
CC standard chemotherapeutic agents. A claimed method of human cancer
CC treatment involves contacting haematopoietic cells from a patient with
CC one or more superantigens ex vivo to generate stimulated cells, selecting
CC a specific V beta subset of cells, and reintroducing these cells into the
CC patient to induce an in vivo therapeutic, tumouricidal reaction
XX
SQ Sequence 221 AA;
Query Match 23.9%; Score 296.5; DB 5; Length 221;
Best Local Similarity 35.6%; Pred. No. 3.7e-21;
Matches 80; Conservative 42; Mismatches 84; Indels 19; Gaps 10;
QY 16 SELQNAL-SNLRQIYY-YNEKAIT-ENKESDDQPLENTLLFKGFTGHPWYNLLVDLG 72
DB 7 SGLHRSSLVKLNQNIYFLYEGDPVTNENKVSVDQLLSHDLIYN---VSGPNYDKLTKELK 63
QY 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEKKVPIINLWI 131
DB 64 NOEWATLFDKNVDIYGVYHLCVCLNARSACIYGGVTNHNHLEIPKIVKRVSI 123
QY 132 DGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGVLFVHSEGG 191
DB 124 DGIO-SLSFD-IETNKKMVAQELDYKVRKYLTDNKQLYTNGP--SKYETGVKIFPKNK 179
QY 192 STVSYDLFD---AQGYPTDLLRIYRDNKTINSENHLIDLYLT 232
DB 180 ESFWFDLPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 220
RESULT 81
AAW12151
ID AAW12151 standard; protein; 251 AA.
XX
AC AAW12151;
XX
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Cys87Ser.
XX

KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fascitis;
XX liver damage; T cell; lymphoma; ovarian; uterine.
OS Streptococcus pyogenes.
XX Synthetic.
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Peptide /label= mat_peptide
FT Misc-difference 117
FT /note= "wild type Cys replaced by Ser"
XX
FN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX WPI; 1997-099936/09.
DR
XX Mutant SPE-A toxin with at least one amino acid change is substantially
XX non-lethal - used in vaccine composition for treatment of cancer and
XX streptococcal toxic shock syndrome etc.
XX
XX Example 4; Page; 102pp; English.
PS
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fascitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;
Query Match 23.9%; Score 296.5; DB 2; Length 251;
Best Local Similarity 34.3%; Pred. No. 4.4e-21;
Matches 82; Conservative 44; Mismatches 90; Indels 23; Gaps 11;
QY 4 SEENEXDLRKKSLQNAL-SNLRQIYY-YNEKAIT-ENKESDDQPLENTLLFKGFTG 60
DB 25 SQEVAQDDPPDPSQLHRSSLVKLNQNIYFLYEGDPVTNENKVSVDQLLSHHLIYN---VS 81
QY 61 HPWYNLLVDLIGSKDATNKYKGVLDLYGAYY---GYQCAGGTPNKTACMYGGVTLHDNN 117
DB 82 GPNYDKLTKELKNQEMATLFDKNVDIYGVYHLSYLCENA--ERSACIYGGVTNHN 139
QY 118 RLTEKKVPIINLWIDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGLYNSDSFGG 177
DB 140 HLEIPKIVKVSIDGIQ-SLSFD-IETNKKMVAQELDYKVRKYLTDNKQLYTNGP--S 195
QY 178 KVQGLVIFHSSEGSTVSYDLFD---AQGYPTDLLRIYRDNKTINSENHLIDLYLT 232
DB 196 KYETGYIKFIPKNKESFWDFPPEFTQSKY----LMIYKDNETLDSNTSQIEVLYLT 250


```
QY 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQC-AGGTPNKTACWYGVVTLHDNNRL 119
Db 82 GPNYDKLKTENKQEMATLFDKKNVDIYGVYHLCYLCENASACTYGGVTNHEGNHL 141
QY 120 TEEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGRFGLYNSDSFGGKV 179
Db 142 EIPKKIVVKVSDIGIQ-SLSFD-IETNKKMVTAGELDYKVRKYLTDNKKLYTNGP--SKY 197
QY 180 QRGIVFHSSSGSTVSVDLFD----AQQYPTDLLRIYRDNKTINSENLHIDLXYLT 232
Db 198 ETGYIKFIPKNKESFWDFPPEPTQSKY----LMIYKONETLDSNTSQIEVYLTT 250

RESULT 84
AAW12154
ID AAW12154 standard; protein; 251 AA.
XX
AC AAW12154;
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Ser195Ala.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Misc-difference 225 /label= mat_peptide
FT /note= "wild type Ser replaced by Ala"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Example 4; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fasciitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
```

```
XX SQ Sequence 251 AA;
Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 7.1e-21;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEEINEKDLRKKSELORNAL-SNLRQIYY-YNEKAIT-ENKESDDQFLENTLLFKGPFPTG 60
Db 25 SQEFAQODPDPQSQRHSSSLVKNLQNIYFLYEGDPVTHENVKSVQDLLSHHLYN---VS 81
QY 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYGYQC-AGGTPNKTACWYGVVTLHDNNRL 119
Db 82 GPNYDKLKTENKQEMATLFDKKNVDIYGVYHLCYLCENASACTYGGVTNHEGNHL 141
QY 120 TEEKKVPINLWIDGKQTTPIDKVKTSKKEVTVQELDLQARHYLHGRFGLYNSDSFGGKV 179
Db 142 EIPKKIVVKVSDIGIQ-SLSFD-IETNKKMVTAGELDYKVRKYLTDNKKLYTNGP--SKY 197
QY 180 QRGIVFHSSSGSTVSVDLFD----AQQYPTDLLRIYRDNKTINSENLHIDLXYLT 232
Db 198 ETGYIKFIPKNKESFWDFPPEPTQAKY----LMIYKONETLDSNTSQIEVYLTT 250

RESULT 85
AAW12146
ID AAW12146 standard; protein; 251 AA.
XX
AC AAW12146;
DT 04-NOV-1997 (first entry)
XX
DE Streptococcus pyogenes Streptococcal toxin A mutant Lys157Glu.
XX
KW Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
KW protection; treatment; cancer; neutralising antibody;
KW streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
KW hypotension; group A streptococcal infection; myositis; fasciitis;
KW liver damage; T cell; lymphoma; ovarian; uterine.
XX
OS Streptococcus pyogenes.
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Peptide 1..30
FT Peptide /label= sig_peptide
FT Peptide 31..251
FT Misc-difference 187 /label= mat_peptide
FT /note= "wild type Lys replaced by Glu"
XX
PN WO9640930-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US010252.
XX
PR 07-JUN-1995; 95US-00480261.
XX
PA (MINU ) UNIV MINNESOTA.
XX
PI Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
XX
DR WPI; 1997-099936/09.
XX
PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.
XX
PS Claim 5; Page; 102pp; English.
XX
CC The present sequence is a non-lethal Streptococcus pyogenes Streptococcal
CC toxin A (SPE-A) mutant, which can be used to produce vaccines to protect
```

CC animals against wild type SPE-A and to treat cancer and streptococcal
CC toxic shock syndrome (STSS). The mutant SPE-A causes neutralising
CC antibodies (Ab) to be produced, which may be used to ameliorate STSS
CC symptoms, e.g. fever, hypotension, group A streptococcal infection,
CC myositis, fascitis and liver damage. The neutralising Ab is preferably
CC administered in conjunction with antibiotic therapy. The mutant SPE-A is
CC especially useful for treating T cell lymphomas, and ovarian and uterine
CC cancer. It is thought that mutant SPE-A can be selectively toxic to T
CC cell lymphoma cells. N.B. Sequence not given in the specification, but
CC constructed using the wild type SPE-A sequence given on pages 77-79
XX
SQ Sequence 251 AA;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 7.1e-21;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
QY 4 SSEEINEKDLRKXSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
DB 25 SQEVAQQDDPDSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYN---VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGTPTNKTACMYGGVTLHDNNRL 119
DB 82 GPNYDKLKTTELKNQEMATLFDKQNDVIYGVYVYHLCLCENAEARSACIYGGVTNHEGNHL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
DB 142 EIPKIVKVSIDGIG-SLSPD-IETNKKQVTAQELDYKVRKYLTDNEQLYNGP--SKY 197
QY 180 QRLIVFHSSEGSTVSYDLFD----AQGYPTDTLRIYRDNKTINSENLHIDLTYLT 232
DB 198 ETGYIKFIPKNKESFWDFPFPEPTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250

RESULT 86
AAW12097
ID AAW12097 standard; protein; 251 AA.
AC AAW12097;
XX
XX 04-NOV-1997 (first entry)

Streptococcus pyogenes Streptococcal toxin A.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
protection; treatment; cancer; neutralising antibody;
streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
hypotension; group A streptococcal infection; myositis; fascitis;
liver damage; T cell; lymphoma; ovarian; uterine.

Streptococcus pyogenes.

Key Location/Qualifiers
FT Peptide 1..30 /label= sig_peptide
FT Peptide 31..251 /label= mat_peptide
FT

W09640930-AL.

19-DEC-1996.

07-JUN-1996; 96WO-US010252.

07-JUN-1995; 95US-00480261.

(MINU) UNIV MINNESOTA.

Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;

WPI; 1997-099936/09.

N-PSDB; AAW12097.

XX

PT Mutant SPE-A toxin with at least one amino acid change is substantially
PT non-lethal - used in vaccine composition for treatment of cancer and
PT streptococcal toxic shock syndrome etc.

XX Disclosure; Page 77-79; 102pp; English.

CC The present sequence is Streptococcus pyogenes Streptococcal toxin A (SPE
CC -A), from which a non-lethal mutant SPE-A, comprising at least 1 amino
CC acid change, can be derived. The mutant SPE-A can be used to produce
CC vaccines to protect animals against wild type SPE-A and to treat cancer
CC and streptococcal toxic shock syndrome (STSS). The mutant SPE-A causes
CC neutralising antibodies (Ab) to be produced, which may be used to
CC ameliorate STSS symptoms, e.g. fever, hypotension, group A streptococcal
CC infection, myositis, fascitis and liver damage. The neutralising Ab is
CC preferably administered in conjunction with antibiotic therapy. The
CC mutant SPE-A is especially useful for treating T cell lymphomas, and
CC ovarian and uterine cancer. It is thought that mutant SPE-A can be
CC selectively toxic to T cell lymphoma cells

XX Sequence 251 AA;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 34.2%; Pred. No. 7.1e-21;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SSEEINEKDLRKXSELQNAL-SNLRIQIYY-YNEKAIT-ENKESDDQFLENTLLFKGFFTG 60
DB 25 SQEVAQQDDPDSQLHRSLSLVKNLQNIYFLYEGDPVTHENVKSVQDQLSHHLLIYN---VS 81
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGTPTNKTACMYGGVTLHDNNRL 119
DB 82 GPNYDKLKTTELKNQEMATLFDKQNDVIYGVYVYHLCLCENAEARSACIYGGVTNHEGNHL 141
QY 120 TEEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYNSDSFGKV 179
DB 142 EIPKIVKVSIDGIG-SLSPD-IETNKKQVTAQELDYKVRKYLTDNEQLYNGP--SKY 197
QY 180 QRLIVFHSSEGSTVSYDLFD----AQGYPTDTLRIYRDNKTINSENLHIDLTYLT 232
DB 198 ETGYIKFIPKNKESFWDFPFPEPTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250

RESULT 87
AAW12147

ID AAW12147 standard; protein; 251 AA.

AC AAW12147;
XX
XX 04-NOV-1997 (first entry)

Streptococcus pyogenes Streptococcal toxin A mutant Asn20Aep.

Streptococcal; toxin A; SPE-A; non-lethal; mutant; production; vaccine;
protection; treatment; cancer; neutralising antibody;
streptococcal toxic shock syndrome; STSS; symptom; amelioration; fever;
hypotension; group A streptococcal infection; myositis; fascitis;
liver damage; T cell; lymphoma; ovarian; uterine.

Streptococcus pyogenes.

Synthetic.

Key Location/Qualifiers
FT Peptide 1..30 /label= sig_peptide
FT Peptide 31..251 /label= mat_peptide
FT Misc-difference 50 /note= "wild type Asn replaced by Asp"

W09640930-AL.

19-DEC-1996.

XX

XX SPE-A toxin; nonlethal; mutant; Streptococcus pyogenes exotoxin A;
 KW wild type; nontoxic; antibody; vaccine; immunity; ovarian cancer;
 KW streptococcal toxic shock syndrome; STSS; T cell lymphoma;
 KW uterine cancer.
 XX Streptococcus pyogenes.
 OS WO9824911-A2.
 XX
 XX
 PD 11-JUN-1998.
 XX
 XX 05-DEC-1997; 97WO-US022228.
 PF
 XX 06-DEC-1996; 96US-0032930P.
 PR
 XX (MINU) UNIV MINNESOTA.
 PA
 XX Schlievert PM, Roggiani M, Stoehr J, Ohlendorf D;
 PI
 XX WPI; 1998-333330/29.
 DR
 DR N-PSDB; AAV41593.
 XX
 XX New mutant Streptococcal SPE-A toxins - useful for, e.g. prevention or
 PT treatment of streptococcal infection or toxic shock syndrome.
 PT
 XX Disclosure; Fig 3; 95pp; English.
 PS
 XX This is the amino acid sequence of the Streptococcus pyogenes exotoxin A
 CC (SPE-A toxin). The novel mutant Streptococcal SPE-A toxin has at least 1
 CC aa change and is nonlethal compared with a protein to wild type SPE-A
 CC toxin. The mutant SPE-A toxins are nontoxic and can produce antibodies
 CC that neutralise wild type SPE-A toxin activity. The toxins can be used in
 CC vaccines and therapeutics to generate a protective immune response
 CC against streptococcal infection. They can be used to protect against the
 CC development of streptococcal toxic shock syndrome (STSS). In addition,
 CC the toxins can be used for treating animals with symptoms of
 CC streptococcal infection or STSS and in methods for stimulating T cell
 CC proliferation and in the treatment of cancer. In particular they can be
 CC used for treating T cell lymphomas, and ovarian and uterine cancer.
 CC
 SQ Sequence 251 AA;
 XX
 Query Match 23.8%; Score 294.5; DB 2; Length 251;
 Best Local Similarity 34.2%; Pred. No. 7.1e-21;
 Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;
 QY 4 SEEINEKDLRKSELRNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTTG 60
 DB 25 SQEVAQQDPDPQLSRSSLVNQLNIYFLYEGDPVTHENVKSVDDQLLSHLIYN---VS 81
 QY 61 HPWYNDLLVGLGSKDATNKYKGGVDLYGAYGYQC-AGGTPNKTCMYGGVTLHDNNRL 119
 DB 82 GPNYDKLTKLNQEMATLFDKQNDVIYGVYHLCLCENAEARSACIYGGVTNHEGHL 141
 QY 120 TEEKKVPINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVV 179
 DB 142 EIPKIVKVSIDGIQ-SLSFD-IETKQNVTAQELDYKVKYLTNDKQLYTNGP--SKY 197
 QY 180 QRGLIVFHSSEGSTVSVDLFD-----AQGYVPTLLRIYRDNKTINSENLHIDLYLT 232
 DB 198 ETGYIKFIPKNKESFWDFPEPEFTQSKY----LMIYKDNELTDSNTSQIEVLYLT 250
 RESULT 90
 AAY06254
 ID AAY06254 standard; protein; 239 AA.
 XX
 AC AAY06254;
 XX
 XX 23-AUG-1999 (first entry)
 DT
 XX Staphylococcal group C enterotoxin SEC3-FRI909.
 DE

XX Enterotoxin; SEC3-FRI909; toxin; disulfide loop; protein engineering.
 KW Staphylococcus aureus.
 OS
 XX Key Location/Qualifiers
 FT Disulfide-bond 93..110
 XX WO9927889-A2.
 PN
 XX 10-JUN-1999.
 PD
 XX 01-DEC-1998; 98WO-US025107.
 PF
 XX 02-DEC-1997; 97US-0067357P.
 PR
 XX (IDAH-) IDAHO RES FOUND INC.
 PA
 XX Bohach GI;
 PI
 XX WPI; 1999-358008/30.
 DR
 DR Non-toxic modified staphylococcal enterotoxins.
 XX
 PT Disclosure; Page 17; 25pp; English.
 PS
 XX This protein represents the Staphylococcus aureus type C enterotoxin SEC3
 CC -FRI909. The invention relates to pyrogenic toxins, such as
 CC staphylococcal enterotoxins, modified in the disulfide loop region.
 CC Typically, the modification involves deletions within the disulfide loop
 CC region of SEC (see AAY06261). The modified toxins retain useful
 CC biological properties, such as the ability to induce cytokine production,
 CC but have substantially reduced toxicity compared to the corresponding
 CC unmodified native toxin. Emetic response inducing activity and fever
 CC inducing activity are typically decreased by at least about 100-fold,
 CC while LD50 (in Dutch Belted rabbits) is at least 100-fold higher than the
 CC native toxin
 CC
 SQ Sequence 239 AA;
 XX
 Query Match 23.7%; Score 293.5; DB 2; Length 239;
 Best Local Similarity 33.3%; Pred. No. 8.3e-21;
 Matches 78; Conservative 48; Mismatches 89; Indels 19; Gaps 9;
 QY 11 DLRKSELRNALSLROIYYNEKAITENK-ESDDQFLENTLLPKGFTTGHWPYNDLLV 69
 DB 10 DLHKSEEF-TGTWGNMK--LYDDHVVSATKVSVDKFLAHLIYNINDKLNNDKVKVT 66
 QY 70 DLGSKDATNKYKGGVDLYGAYGYQC-----AGGTENKTCMYGGVTLHDNNRLTEE 122
 DB 67 ELLNEDLANKYKDEVVDVYVGSNYVNCYFSSKDNVGVKTSKGTTCMYGGITKIEGHNFDNG 126
 QY 123 --KKVPIINLWIDGKQTTVPIDKVTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKVV 180
 DB 127 NLQNVLLIRY-ENKRNITISFE-VQDKSVTAQELDIKARNFINKNLNLYEFNS--SPYE 182
 QY 181 RGLIVFHSSEGSTVSVDLFDQAQGYPD--TLRIYRDNKTINSENLHIDLYLT 232
 DB 183 TGYIKFIESNGTTFWYDMMPAFGDKFDQSKLMYIKDNKMWDSKSVKIEVHLTT 236
 RESULT 91
 ABG71370
 ID ABG71370 standard; protein; 240 AA.
 XX
 AC ABG71370;
 XX
 XX 29-JAN-2003 (first entry)
 DT
 XX Staphylococcal enterotoxin SEC3-FRI909.
 DE
 XX Modified pyrogenic toxin; disulfide loop; fever-inducing activity;
 KW emetic response-inducing activity; staphylococcal enterotoxin;
 DE

KW toxic shock syndrome; food poisoning; immunostimulant; antibacterial;
 KW SEC3-FR1909.
 OS Staphylococcus aureus.
 FH Key Location/Qualifiers
 FT Misc-difference 240
 FT /label= unknown
 XX WO200283169-A1.
 XX 24-OCT-2002.
 XX 11-APR-2002; 2002WO-US011619.
 XX 13-APR-2001; 2001US-0283720P.
 XX (IDAH-) IDAHO RES FOUND INC.
 XX Marshall MJ, Shiel PJ, Berger PH, Bohach GA, Bohach CH;
 XX WPI; 2003-058608/05.
 XX New modified staphylococcal enterotoxin derived from a native disulfide
 PT loop-containing pyrogenic toxin, useful for non-specifically enhancing an
 PT immune function and as a vaccine against toxic shock syndrome or food
 PT poisoning.
 XX Disclosure; Fig 15; 67pp; English.
 XX The invention relates to a modified pyrogenic toxin derived from a native
 CC disulphide loop-containing pyrogenic toxin where the modified toxin
 CC comprises a disulphide loop having no more than 10 amino acids. The
 CC modified toxin has a fever-inducing activity or an emetic response-
 CC inducing activity decreased by about 100-fold in comparison to a native
 CC toxin. The modified pyrogenic toxin, that is a staphylococcal
 CC enterotoxin, is useful for non-specifically enhancing an immune function
 CC and for vaccination against diseases such as toxic shock syndrome and
 CC food poisoning. This sequence represents the staphylococcal enterotoxin,
 CC SEC3-FR1909
 XX SQ Sequence 240 AA;

Query Match 23.7%; Score 293.5; DB 6; Length 240;
 Best Local Similarity 33.3%; Pred. No. 8.3e-21;
 Matches 78; Conservative 48; Mismatches 89; Indels 19; Gaps 9;

Qy 11 DLKSKSELQARNALNRQIYYNNEKAITENK-ESDDQFLENTLLFKGFTTGHWPYNLLV 69
 Db 10 DLKSEEF-TGTGCMNK--LYDDHYVSATKVKSVDRFLAHDLYINNDKLNNDYKVT 66

Qy 70 DLGSKDATNKYKGVLDLYGAYGYQC-----AGTPTNKATACMGVTLHDNRLTEE 122
 Db 67 ELLNEDLANKYKDEVDVYGSNYVNCYFSSKDNVGVTSKTKCMYGGITKHGHNFDNG 126

Qy 123 --KVPINLWDGKQTTVPIDKVTSKKEVTVOELDLQARHLHGKFGLYNSDSFGGKVQ 180
 Db 127 NLQVNLIRVY-ENKRNITISFE-VQTDKKSVAQAELDIKARNFLNKNLYEFNS--SPYE 182

Qy 181 RGLIVFHSSEGSTVSYDLFDAQQGYPD--TLRLIYRDNKNTINSENHLIDL 232
 Db 183 TGYIKFTIESNGTWFYDMMPPAGPKFDQSKYLMYKDKMVDKSKVIEVHLT 236

RESULT 92
 ABB79503
 ID ABB79503 standard; protein; 266 AA.
 XX ABB79503;
 AC ABB79503;
 XX 23-SEP-2002 (first entry)
 XX Staphylococcal enterotoxin B vaccine (B42360210).
 DE

XX Enterotoxin B; superantigen; antigen; toxin; vaccine; B42360210;
 KW attenuation.
 OS Staphylococcus sp.
 XX US6399332-B1.
 XX 04-JUN-2002.
 XX 01-SEP-1998; 98US-00144776.
 XX 25-JUN-1997; 97US-00882431.
 XX (USSA) US SEC OF ARMY.
 XX Ulrich RG, Olson MA, Bavari S;
 XX WPI; 2002-546281/58.
 XX N-PSDB; ABN84224.
 XX Novel isolated and purified superantigen toxin DNA fragment which has
 PT been genetically altered, useful for producing vaccine for treatment of
 PT superantigen toxin-associated bacterial diseases.
 XX Disclosure; Col 41-43; 46pp; English.
 XX The present sequence is the protein sequence of staphylococcal
 CC enterotoxin B (SEB) vaccine B42360210. The invention relates to a vaccine
 CC against superantigen toxin-associated bacterial diseases. Superantigen
 CC vaccines were developed by engineering changes in the receptor-binding
 CC portions of superantigen toxins such as SEB to reduce receptor-binding
 CC affinities and toxicity while maintaining antigenicity. In examples from
 CC the invention, attenuated superantigen toxins were shown to protect
 CC animals against challenge with wild-type toxin. Methods of producing and
 CC using the altered superantigen toxins as vaccines, and in diagnosis and
 CC therapy, are provided. A multivalent vaccine consisting of altered
 CC superantigen toxins from SEA, SEB, SEC-1, TSST-1 and streptococcal SPEA
 CC is predicted to provide protective immunity against the majority of
 CC bacterial superantigen toxins
 XX SQ Sequence 266 AA;

Query Match 23.7%; Score 293.5; DB 5; Length 266;
 Best Local Similarity 32.8%; Pred. No. 9.7e-21;
 Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;

Qy 1 SEKSEETNEKDLRKKSBLQRNALSNLRQIYYNNEKAITENKESDDQFLENTLLFKGFTT 60
 Db 27 AESQDPKPDDELHKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLIYSIKDTK 84

Qy 61 HPWYNDLLVLDGSKDATNKYKGVLDLYGAYGYQC-----AGTPTNKATACMGV 110
 Db 85 LGDYDNRVRFKNDKADKDKYDVFVGANYYYQCYFSSKNTDINSHQTDKRTKCMYGG 144

Qy 111 VTLDHNNRLTEKKVPINLWIDGKQTTVPIDKVTSKKEVTVOELDLQARHLHGKFGLY 170
 Db 145 VTEHNGQLDKYRITVRVVEDGK-NLLSEF-VQTNKKVTAQAELDYLTRHLVKNKKLY 202

Qy 171 NSDSFGGKVGRLIVFHSSEGSTVSYDLFDAQQG--YPTLLRIYRDNKNTINSENHLIDL 228
 Db 203 EFNN--SPYETGYIKFTIENENS-FWYDMMPPAGPKFAQSKYLMYNDKMKVDKVKIEV 259

Qy 229 YLYT 232
 Db 260 YLTT 263

RESULT 93
 ABU10083
 ID ABU10083 standard; protein; 266 AA.
 XX ABU10083;
 AC ABU10083;


```
XX 11-AUG-2003 (first entry)
XX ABU62326
DE Staphylococcal enterotoxin B #1.
XX Enterotoxin B; superantigen-associated bacterial infection; vaccine;
KW superantigen toxin.
XX Staphylococcus sp.
OS US2003009015-A1.
XX 09-JAN-2003.
XX 25-JUN-1997; 97US-00882431.
XX 25-JUN-1997; 97US-00882431.
XX (ULRI/) ULRICH R G.
PA (OLSO/) OLSON M A.
PA (BAVA/) BAVARI S.
PI Ulrich RG, Olson MA, Bavari S;
XX WPI; 2003-401542/38.
DR N-PSDB; ACA61179.
XX New superantigen toxin and/or DNA fragment with an altered binding of the
PT encoded altered toxin to either MHC class II or T cell antigen receptor,
PT useful for treating or ameliorating superantigen-associated bacterial
PT infection.
XX Claim 12; Page 23-24; 50pp; English.
XX The invention relates to an isolated and purified superantigen toxin
CC and/or DNA fragment, which has been altered so that the binding of the
CC encoded toxin to either major histocompatibility complex (MHC) class II
CC or T cell antigen receptor is altered. The superantigen toxins, DNA
CC fragments, and vaccines are useful for treating or ameliorating
CC superantigen-associated bacterial infection. The DNA fragments are
CC particularly useful for producing vaccine against superantigen toxin
CC infections. The transformed host cells are useful for analysing the
CC effectiveness of drugs and agents that affect the binding of
CC superantigens to MHC class II or T-cell antigen receptors. The present
CC sequence represents the amino acid sequence of staphylococcal enterotoxin
CC B #1
XX Sequence 266 AA;
XX Query Match 23.7%; Score 293.5; DB 6; Length 266;
XX Best Local Similarity 32.8%; Pred. No. 9.7e-21;
XX Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLFPKGF 60
DB 27 AESQDPKPDHLKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLYISKDTK 84
QY 61 HPWYNDLLVGLSGDATNKYKGVLYGAYGYQC-----AGTTPNKTACMYGG 110
DB 85 LGDYDNVRVEFKNLADKYDVDFGANYYYQCYFSKKTINDINSHQDKRKTMYGG 144
QY 111 VTLDNNRLTEKKVPINLWIDGQTTVPIDKVKTSKEVTVOELDLQARHYLHGRFGLY 170
DB 145 VTEHNGQLDKYSITVRVEDGK-NLLSFD-VQTNKKKTAQELDYLTREHYLVKNKLY 202
QY 171 NSDSFGKVGQRIIVFHSSEGSTVSVYDLFDAQGQ--YPTDLLRIYRDNKNTINSENLHIDL 228
DB 203 EFNN--SPYETGYIKFIENENS-FWYDMPAPGDKFAQSKYLMWYNDNKNMVDKDKVIEV 259
QY 229 YLYT 232
DB 260 YLTT 263
```

```
RESULT 94
ABU62326
ID ABU62326 standard; protein; 266 AA.
XX AC ABU62326;
XX DT 27-AUG-2003 (first entry)
XX DE S. aureus wild-type enterotoxin B, SEB.
XX KW SEB; staphylococcal enterotoxin B; vaccine; superantigen toxin; MHC;
KW superantigen-associated bacterial infection; bacterial infection;
KW antibacterial.
XX OS Staphylococcus aureus.
XX FH Key Location/Qualifiers
FT Peptide 1..27
FT Protein /label= Signal_peptide
FT /label= Mature_SEB
XX US2003036644-A1.
XX 20-FEB-2003.
XX 26-NOV-2001; 2001US-00002784.
XX 25-JUN-1997; 97US-00882431.
XX 01-SEP-1998; 98US-0014776.
XX (ULRI/) ULRICH R G.
XX Ulrich RG;
XX WPI; 2003-492125/46.
XX N-PSDB; ACD28896.
XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX Disclosure; Page 26-27; 68pp; English.
XX The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antiserum isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents wild-type SEB
XX Sequence 266 AA;
XX Query Match 23.7%; Score 293.5; DB 7; Length 266;
XX Best Local Similarity 32.8%; Pred. No. 9.7e-21;
XX Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
QY 1 SEKSEINEKDLRKKSSELOQNALSNLRQIYYNEKAITENKESDDOFLNTLFPKGF 60
DB 27 AESQDPKPDHLKSKF--TGLMEDMKVLYDDNHVSAINVKSIDQFLYFDLYISKDTK 84
```

Qy 61 HPWYNDLIVDLSGSDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144
Qy 111 VTLDHNNRLTEBEKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKVQRLVHFSSEGSTVSVDLFDAGQ--YPTDTLRIYRDNKTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNMVDSDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
RESULT 95
AAE37678
ID AAE37678 standard; protein; 266 AA.
XX AC AAE37678;
XX DT 06-OCT-2003 (first entry)
XX DE Protein #3 related to the invention.
XX KW Superantigen toxin; vaccine; infection; gene therapy.
XX OS Unidentified.
XX PN WO2003056015-A1.
XX PD 10-JUL-2003.
XX PF 26-NOV-2001; 2001WO-US046540.
XX PR 26-NOV-2001; 2001US-00002784.
XX FA (USME-) US MEDICAL RES INST INFECTIOUS DISEASES.
XX PI Ulrich RG;
XX DR WPI; 2003-492125/46.
XX DR N-PSDB; AAD56766.
XX PT New superantigen toxin DNA fragment, useful for preparing a composition
XX PT for treating or preventing bacterial infection.
XX PS Disclosure; Page 114-115; 141pp; English.
XX CC The invention provides a superantigen toxin DNA fragment which has been
XX CC genetically altered such that binding of the encoded altered toxin to
XX CC either the MHC class II or T cell antigen receptor is disrupted or
XX CC altered. DNA fragments of the invention are useful in the production of
XX CC vaccines against bacterial superantigen toxin infections. They are also
XX CC useful in gene therapy. The present sequence is a protein related to the
XX CC invention
SQ Sequence 266 AA;
Query Match 23.7%; Score 293.5; DB 7; Length 266;
Best Local Similarity 32.8%; Pred. No. 9.7e-21;
Matches 80; Conservative 45; Mismatches 100; Indels 19; Gaps 7;
Qy 1 SEKSEINEKDLRKXSELRNALSLRQIYYNYNEKAITENKESDDQFLENTLLFKGFTG 60
Db 27 AESQDPKPEDELHKSSKP--TCLMEDMKVLVDNHNHVSAINVKSIDQFLYFDLIYSIKDTK 84
Qy 61 HPWYNDLIVDLSGSDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGG 110
Db 85 LGDYDNVRVEFNKDLADKYKDYVDFGANYYYQCYFSKKTNDINSHQTDKRTCMYGG 144

Qy 111 VTLDHNNRLTEBEKVPINLWIDGQTTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLY 170
Db 145 VTEHNGNQLDKYRSITVRVFDGK-NLLSPD-VQTNKKKVTQAQELDYLTRHYLVKNKKLY 202
Qy 171 NSDSFGGKVQRLVHFSSEGSTVSVDLFDAGQ--YPTDTLRIYRDNKTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMPAPGDKFAQSKYLMYNDNKNMVDSDVKIEV 259
Qy 229 YLYT 232
Db 260 YLTT 263
RESULT 96
AAB67344
ID AAB67344 standard; peptide; 221 AA.
XX AC AAB67344;
XX DT 23-APR-2001 (first entry)
XX DE Streptococcus pyogenes toxin A protein.
XX KW Tumour; cancer; immune; enterotoxin.
XX OS Streptococcus pyogenes.
XX PN US6180097-B1.
XX PD 30-JAN-2001.
XX PF 30-OCT-1998; 98US-00183437.
XX PR 03-OCT-1989; 89US-00416530.
XX PR 17-JAN-1990; 90US-00466577.
XX PR 17-JAN-1991; 91WO-US000342.
XX PR 01-JUN-1992; 92US-00891718.
XX PR 02-MAR-1993; 93US-00025144.
XX PR 31-JAN-1994; 94US-00189424.
XX PR 19-JUN-1995; 95US-00491746.
XX FA (TERM/) TERMAN D S.
XX PI Terman DS;
XX XX WPI; 2001-158657/16.
XX PT Tumor cell capable of stimulating antitumor immune reactivity in vitro or
XX PT in vivo comprises exogenous nucleic acids encoding a superantigen and a
XX PT costimulatory molecule.
XX PS Disclosure; Fig 2; 16pp; English.
XX CC The present invention relates to a tumour cell capable of stimulating
XX CC antitumor immune reactivity in vitro or in vivo contains and expresses an
XX CC exogenous nucleic acid molecule encoding a superantigen or its active
XX CC fragment and an exogenous nucleic acid molecule encoding a costimulatory
XX CC molecule that activates T cells in conjunction with an antigenic
XX CC stimulus. The invention may be used for cancer therapy by stimulating an
XX CC anticancer immune response in vivo or ex vivo
SQ Sequence 221 AA;
Query Match 23.6%; Score 292.5; DB 4; Length 221;
Best Local Similarity 35.1%; Pred. No. 9.3e-21;
Matches 79; Conservative 42; Mismatches 85; Indels 19; Gaps 10;
Qy 16 SELORNAL-SNLROIYY-YNEKAIT-ENKESDDQFLENTLLFKGFTGHPWYNDLVDLG 72
Db 7 SOLHRSSVLKQLNIYFLYEGDPVTHENVKSVQDLLSHDLIN---VSGPNVDKLTCLK 63
Qy 73 SKDATNKYKGVLDLYGAYGYQC-AGGTPNKTACMYGGVTLHDNNRLTEBEKVPINLWI 131

```

Db 64 NOEMATLFGKKNVDYGVVEYHLCYLCEAERSACIYGGVTNHEGNHLEIPKKIIVKVSIG 123
QY 132 DCKQTTVPIDKVKTSKEVTVQELDLQARHYLHGRKFLYNSDSFGKQVORGVLIVFHSSEG 191
Db 124 DGIQ-SLSPD-IETNKKWTAQELDYKVRKYLTDNKQLYTNGP--SKYETGYIKFIPKMK 179
QY 192 STVSVDLFD----AQQYPTLLRIYRDNKTINSENHLHIDLYLT 232
Db 180 ESFWDFPPEPTQSKY----LMIYKDNETLDSNTSQIEVYLTT 220

RESULT 97
AAR13206
ID AAR13206 standard; protein; 239 AA.
XX
AC AAR13206;
XX
DT 15-OCT-1991 (first entry)
XX
DE Staphylococcal enterotoxin B.
XX
KW SEB; cancer treatment; pyrogen; tumouricide.
XX
OS Staphylococcus aureus.
XX
PN W09110680-A.
XX
PD 25-JUL-1991.
XX
PF 17-JAN-1990; 90US-00466577.
XX
PR 17-JAN-1990; 90US-00466577.
XX
PA (TERM/) Terman D S.
XX
PI Terman DS;
XX
WPI; 1991-237984/32.
XX
PT Treating cancer with enterotoxin from Staphylococcus aureus -
PT administered by IV injection, having same tumoricidal activity as
PT Staphylococcal protein A without potential toxic reactions.
PS Disclosure; Fig 1; 74pp; English.
CC SEB was isolated and purified from S. aureus. It can be used for treating
CC cancer, activating cytokine mediators and procoagulant systems,
CC augmenting natural killer cell cytotoxicity, etc. The enterotoxin can be
CC administered intravenously, optionally with ibuprofen to attenuate toxic
CC reaction to SEB. Synthetic polypeptides having structural homology to
CC Staphylococcal exotoxins are claimed, provided the homology includes
CC statistically significant sequence homology, alignment of Cysteine
CC residues and similar hydropathy profiles. See AAR13203-R13211
XX
SQ Sequence 239 AA;

```

```

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-20;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKKELQARNLSNRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPDDELHKSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNLDLLVGLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGV 111
Db 59 GNYDNRVRFKNDLADKYDKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGV 118
QY 112 TLHDNRLTEEEKVVPINLWDGKQTTVPIDKVKTSKEVTQELDLQARHYLHGRKFLYN 171
Db 119 TEHNGQLDKYSLTVRVFEDGK-NLLSPD-VQTNKKKVTQAEQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKGKQVORGVLIVFHSSEGSTVSVDLFDQAQGYPD--TLLRIYRDNKTINSENHLHIDLY 229

```

```

QY 172 SDSFGKGKQVORGVLIVFHSSEGSTVSVDLFDQAQGYPD--TLLRIYRDNKTINSENHLHIDLY 229
Db 177 FNN--SPYETGYIKFIENENS-FWYDLMPAPGDKFDQSKYLMNYNDNKMVDSKDVKIEVY 233
QY 230 L 230
Db 234 L 234

RESULT 98
AAR45014
ID AAR45014 standard; protein; 239 AA.
XX
AC AAR45014;
XX
DT 25-MAR-2003 (revised)
DT 08-JUN-1994 (first entry)
XX
DE Staphylococcal enterotoxin SEB.
XX
KW Staphylococcal enterotoxin; SE; cancer; tumouricidal agent;
KW autoimmune disease; toxicity; Protein A; perfusion system.
XX
OS Staphylococcus aureus.
XX
PN W09324136-A1.
XX
PD 09-DEC-1993.
XX
PF 01-JUN-1993; 93WO-US005213.
XX
PR 01-JUN-1992; 92US-00891718.
XX
PA (TERM/) Terman D S.
XX
PA (STON/) STONE J L.
XX
PI Terman DS, Stone JL;
XX
WPI; 1993-405418/50.
XX
PT Use of staphylococcal enterotoxin(s) and homologues - for treating cancer
PT in a patient or for the treatment of auto-immune diseases.
XX
PS Disclosure; Fig 1; 90pp; English.
XX
CC The sequences given in AAR45011-21 are Staphylococcal enterotoxins (SEs)
CC which may be used in the methods of the invention for treating cancer in
CC a patient. These SEs, and homologues of them, can be used as tumoricidal
CC agents for treating cancers and autoimmune disease. They exhibit
CC tumoricidal activity and toxicity identical to that observed for the
CC Protein A perfusion system. They may be administered by i.v. injection.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ Sequence 239 AA;

```

```

Query Match 23.6%; Score 292.5; DB 2; Length 239;
Best Local Similarity 34.0%; Pred. No. 1e-20;
Matches 82; Conservative 44; Mismatches 96; Indels 19; Gaps 8;

QY 2 EKSEINEKDLRKKELQARNLSNRQIYYNEKAITENKESDDQPLENTLLFKGFTGH 61
Db 1 ESQDPKPDDELHKSKF-TGLMENMKVLYDDNHVSAI-NVKSIDQFLYFDLIYSIKDTKL 58
QY 62 PWNLDLLVGLGSKDATNKYKGVLDLYGAYGYQC-----AGGTPNKTACMYGV 111
Db 59 GNYDNRVRFKNDLADKYDKVDVFGANYYYQCYFSKKTNDINSHQTDKRTCMYGV 118
QY 112 TLHDNRLTEEEKVVPINLWDGKQTTVPIDKVKTSKEVTQELDLQARHYLHGRKFLYN 171
Db 119 TEHNGQLDKYSLTVRVFEDGK-NLLSPD-VQTNKKKVTQAEQELDYLTRHYLVKNKKLYE 176
QY 172 SDSFGKGKQVORGVLIVFHSSEGSTVSVDLFDQAQGYPD--TLLRIYRDNKTINSENHLHIDLY 229

```

Db 177 FNN--SPYETGYIKFIENENS-FWYDLMAPGDKFDQSKYLMNYNDKNQVDSKDVKIEVY 233
Qy 230 L 230
Db 234 L 234
RESULT 99
AAY92319
ID AAY92319 standard; protein; 266 AA.
XX
AC AAY92319;
XX
DT 10-AUG-2000 (first entry)
XX
DE Plant-optimized mutant staphylococcal enterotoxin B.
XX
KW Rep; replicase; rescue; replication; vector; gene expression;
KW recombinant protein production; plant; intronless; enterotoxin B.
XX
OS Staphylococcus sp.
OS Synthetic.
FN WO200020557-A2.
XX
XX 13-APR-2000.
XX
PF 07-OCT-1999; 99WO-US0233520.
XX
XX 07-OCT-1998; 98US-0103352P.
PR
XX (UYCO-) UNIV CORNELL BOYCE INST PLANT RES.
PA
XX Mason HS, Palmer KE, Mor TS, Hefferon KL, Arntzen C;
PI
XX WPI; 2000-303756/26.
DR
DR N-ESDB; AAA09240.
XX
XX Nucleic acids comprising a portion of a long intergenic region of a
PT geninivirus genome and a sequence comprising a geninivirus replicase
PT gene, useful for amplifying a gene of interest and overproducing a
PT protein of interest in plants.
XX
PS Example 17; Fig 36; 121pp; English.
XX
XX A pair of nucleic acids comprising a portion of a long intergenic region
CC (LIR) of a geninivirus genome lacking a sequence encoding a geniniviral
CC coat protein, and a nucleic acid comprising a geniniviral replicase gene
CC linked to a fruit ripening-dependent promoter, are new. Strains of
CC Escherichia coli and Agrobacterium tumefaciens transfected with an
CC expression vector containing the nucleic acids and a gene of interest are
CC useful for the production of transgenic plants (or cells). The sequences
CC and methods are useful for amplifying a gene of interest and
CC overproducing a protein of interest in recombinant plants
XX
SQ Sequence 266 AA;
Query Match 23.6%; Score 292.5; DB 3; Length 266;
Best Local Similarity 33.2%; Pred. No. 1.2e-20;
Matches 81; Conservative 47; Mismatches 97; Indels 19; Gaps 8;
Qy 1 SEKSEINEKDLRKSELRNALSRLROIYYVNEKAITENKESDDQPLENTLLPKGPFPTG 60
Db 27 AESQDPKPEDELHKSSKF-TGLMENMKVLYDDNHVSAT-NVKSIDQSIFYDLISIKDTK 84
Qy 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQC-----AGGTNKTACMYGG 110
Db 85 LGNYDNVRFENKKNOLADKYDKYVDVFGANYYCYCFSKKTNNDINSHTQDKRKTMYGG 144
Qy 111 VTLHDNRLTEKKVPINLWDGKQTTVPIDKVKTSKKEVTVOELDLQARHLHGKFGLY 170
Db 145 VTEHNGNOLDKYRSITVRVFDGK-NLLSFD-VQTNKKKVKTAQELDYLTRHYLVNKKKLY 202

Qy 171 NSDSFGKGQVORGLIVFHSSSEGSTVSYDLFDAQQGYPD--TLRLRYRONKNTINSENHLIDL 228
Db 203 EFNN--SPYETGYIKFIENENS-FWYDMMAPGDKFDQSKYLMNYNDKNQVDSKDVKIEV 259
Qy 229 YLYT 232
Db 260 YLYT 263
RESULT 100
ABU62453
ID ABU62453 standard; protein; 266 AA.
XX
AC ABU62453;
XX
DT 27-AUG-2003 (first entry)
XX
DE S. aureus periplasmic enterotoxin B mutant E67Q.
XX
KW SEB; staphylococcal enterotoxin B; mutein; mutant; vaccine;
KW superantigen toxin; MHC; superantigen-associated bacterial infection;
KW bacterial infection; antibacterial.
XX
OS Staphylococcus aureus.
OS Synthetic.
XX
XX Key Location/Qualifiers
FH Peptide 1..26
FT /label= Signal_peptide
FT Protein 27..286
FT /label= Mature_SEB_mutant
FT Misc-difference 93
FT /note= "Wild-type Glu substituted by Gln"
XX
XX US2003036644-A1.
XX
XX 20-FEB-2003.
XX
XX 26-NOV-2001; 2001US-00002784.
PF
XX 25-JUN-1997; 97US-00882431.
PR
XX 01-SEP-1998; 98US-0014776.
XX
XX (ULRI/) ULRICH R G.
XX
XX Ulrich RG;
XX
XX WPI; 2003-492125/46.
DR
XX New superantigen toxin DNA fragment, useful for preparing a composition
PT for treating or preventing bacterial infection.
XX
XX Example 2; Page; 69pp; English.
XX
XX The invention relates to an isolated and purified superantigen toxin DNA
CC fragment is altered so that binding of the encoded altered toxin to
CC either the MHC class II or T cell antigen receptor is altered. Also
CC included are a recombinant DNA construct (comprising a vector and an
CC isolated and purified altered superantigen toxin DNA fragment), a host
CC cell transformed with the recombinant DNA construct, producing altered
CC superantigen toxin, an altered TSST-1 (toxic shock syndrome toxin)
CC superantigen toxin peptide, diagnosing superantigen-associated bacterial
CC infection, a vaccine (comprising an altered superantigen toxin for
CC producing antigenic and immunogenic response resulting in the protection
CC of a mammal against superantigen-associated bacterial infection),
CC treating/ameliorating a superantigen-associated bacterial infection, an
CC antisera isolated from individuals immunised with one or more altered
CC TSST-1 superantigen toxin and an antibody which recognises altered TSST-
CC 1. Also disclosed are mutated staphylococcal enterotoxin A, B, C1 (SEA,
CC SEB, SECI) and streptococcal pyrogenic enterotoxin a and b (SPEa and
CC SPEb). The superantigen toxin DNA fragment is useful for preparing a
CC composition for treating or preventing bacterial infection. The present
CC sequence represents the E67Q (with reference to the mature protein

This Page Blank (use)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 11:00:34 ; Search time 15 Seconds
(without alignments)
1494.567 Million cell updates/sec

Title: US-09-900-766-7

Perfect score: 1238

Sequence: 1 SEKSEINEKDLRKSELR.....RDNKTINSENLHLDLYVT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 200 summaries

Database :

PIR 79:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1238	100.0	257	2 A28179	enterotoxin E prec
2	1023	82.6	257	2 A28664	enterotoxin A prec
3	994	80.3	280	2 C89984	enterotoxin P [imp
4	663	53.6	258	2 A33953	enterotoxin D prec
5	461.5	37.3	258	2 H89968	enterotoxin SeN [i
6	387.5	31.3	260	2 E89969	enterotoxin SeO [i
7	339.5	27.4	242	2 C89969	extracellular ente
8	337	27.2	240	2 G89991	extracellular ente
9	320	25.8	239	2 D89969	enterotoxin SEM [i
10	300.5	24.3	266	1 ENSAB6	enterotoxin B prec
11	295.5	23.9	251	1 S29659	exotoxin type A pr
12	285.5	23.1	266	2 S11885	enterotoxin C3 - S
13	281.5	22.7	266	2 A60114	enterotoxin C-2 pr
14	279.5	22.6	236	2 S18789	exotoxin A precurs
15	277.5	22.4	236	2 S18783	exotoxin type A pr
16	272.5	22.0	236	2 S18786	exotoxin type A pr
17	266.5	21.5	266	1 ENSAC1	enterotoxin C-1 pr
18	255.5	20.6	258	2 G89968	extracellular ente
19	245	19.8	250	1 A26152	streptococcal pyro
20	201	16.2	157	2 A89442	hypothetical prote
21	197	15.9	136	2 A89969	enterotoxin YENT2
22	183.5	14.8	235	2 A30509	exotoxin C precurs
23	144	11.6	62	2 H89941	hypothetical prote
24	123	9.9	133	2 H89969	enterotoxin Yent1
25	113	9.1	232	2 F89807	exotoxin 13 [impor
26	107.5	8.7	234	1 XCSAS1	toxic shock syndro
27	105.5	8.5	234	2 H89992	toxic shock syndro
28	101	8.2	232	2 E89807	exotoxin 12 [impor
29	99.5	8.0	231	2 D89807	exotoxin 11 [impor

30	96	7.8	227	2 G89807	exotoxin 14 [impor
31	94.5	7.6	291	2 G86903	cell shape determi
32	94.5	7.6	631	2 S70908	transferrin-binding
33	94	7.6	203	2 C89803	hypothetical prote
34	94	7.6	226	2 C89806	exotoxin 6 [impor
35	93	7.5	1419	1 DVZQF	multidrug resistanc
36	91	7.4	853	2 G80559	trase-like protein
37	90.5	7.3	194	2 AC1553	B. subtilis YjBK p
38	90	7.3	411	2 A11161	flagellar hook pro
39	90	7.3	411	2 A11520	flagellar hook pro
40	89	7.3	5005	2 F82884	hypothetical prote
41	89	7.2	679	2 G71615	phospholipase A2-1
42	89	7.2	1634	2 C89888	DNA-directed DNA p
43	88	7.1	241	2 C89888	hypothetical prote
44	88	7.1	617	2 E96793	hypothetical prote
45	88	7.1	672	1 S73438	MG032 homolog B01
46	87.5	7.1	241	2 T07067	beta-fructofuranos
47	87.5	7.1	556	2 A11394	arginyl tRNA synth
48	87.5	7.1	1014	2 H71602	protein with DnaJ
49	87	7.0	476	2 H82177	conserved hypothet
50	87	7.0	2167	2 AF1489	cell wall-associat
51	86.5	7.0	856	2 B81399	probable periplasm
52	86.5	7.0	1751	2 A45604	major blood-stage
53	86	6.9	630	2 S78650	DNA endonuclease a
54	86	6.9	1090	2 AG1749	glycosidase homolo
55	86	6.9	1353	2 T27404	hypothetical prote
56	85.5	6.9	556	2 AD1770	arginyl tRNA synth
57	85	6.9	614	2 D86342	hypothetical prote
58	85	6.9	617	2 T10102	diphosphate-fructo
59	85	6.9	1902	1 B44858	lactocapin (EC 3.4
60	84.5	6.8	509	2 S73660	MG288 homolog P02
61	84.5	6.8	573	2 AH1793	ABC transporter, A
62	84.5	6.8	2441	2 D71623	erythrocyte membra
63	84	6.8	227	2 C89808	exotoxin 15 [impor
64	84	6.8	272	2 D86671	transposase of IS1
65	84	6.8	492	2 F70339	glycerol kinase -
66	84	6.8	552	2 T41863	chitinase chi-A or
67	84	6.8	668	2 T44118	penicillin-binding
68	84	6.8	668	2 JQ0773	penicillin-binding
69	84	6.8	668	2 JQ0774	major surface glyc
70	84	6.8	1014	2 T30545	hypothetical prote
71	83.5	6.7	319	2 C81390	GAG protein - yeas
72	83.5	6.7	324	2 T03276	ABC transporter, A
73	83.5	6.7	507	2 S36595	li protein - human
74	83.5	6.7	573	2 AF1418	outer membrane ush
75	83.5	6.7	819	1 I83350	transposase of IS1
76	83	6.7	272	2 C86884	hypothetical prote
77	83	6.7	379	2 C83986	hypothetical prote
78	83	6.7	381	2 C83986	probable transcrip
79	83	6.7	464	2 A71509	hypothetical prote
80	83	6.7	478	2 F90497	transferrin-binding
81	83	6.7	631	2 S70910	hypothetical prote
82	83	6.7	819	2 G69801	hypothetical prote
83	83	6.7	280	2 E71604	uncharacterized pr
84	82.5	6.7	247	2 E97118	exotoxin 9 [impor
85	82.5	6.7	292	2 B89807	exotoxin 9 [impor
86	82.5	6.7	315	2 F64716	p-aminobenzoate sy
87	82.5	6.7	328	2 F64187	hypothetical secre
88	82.5	6.7	333	2 H97273	membrane conserved
89	82.5	6.7	609	2 F90160	putative autotransp
90	82.5	6.7	638	2 AH0340	probable ferric si
91	82.5	6.7	726	2 AB0122	hypothetical prote
92	82	6.6	520	2 D83845	upiquitin-like pro
93	82	6.6	631	2 S55243	DNA-directed RNA p
94	82	6.6	756	2 T05829	tyrocidine synthet
95	82	6.6	2910	2 T28156	exotoxin 8 [impor
96	82	6.6	6486	2 A89807	replication protei
97	81.5	6.6	356	2 A89807	hypothetical prote
98	81.5	6.6	616	1 A40457	protein F53H1.4 [i
99	81.5	6.6	804	2 G90571	hypothetical prote
100	81.5	6.6	1378	2 G88637	hypothetical prote
101	81.5	6.6	1553	2 T18502	hypothetical prote
102	81.5	6.6	1711	2 T18429	hypothetical prote

103 81.5 6.6 1883 2 G82875
104 81.5 6.6 2870 2 H96974
105 81 6.5 299 2 A1193
106 81 6.5 333 2 A95582
107 81 6.5 402 2 A95582
108 81 6.5 528 2 S32307
109 81 6.5 562 2 S01312
110 81 6.5 580 2 S49308
111 81 6.5 616 2 A36094
112 81 6.5 626 2 A98115
113 81 6.5 1021 2 A40805
114 81 6.5 1217 2 T21403
115 81 6.5 1561 2 S06839
116 81 6.5 1997 2 F71607
117 81 6.5 2144 2 A97942
118 81 6.5 2485 1 H71621
119 80.5 6.5 261 2 A84077
120 80.5 6.5 344 2 C81920
121 80.5 6.5 413 2 S95650
122 80.5 6.5 993 2 A97334
123 80.5 6.5 1151 2 A45226
124 80.5 6.5 1427 2 S22695
125 80.5 6.5 1520 2 T23620
126 80.5 6.5 1959 2 A61085
127 80 6.5 276 2 T12558
128 80 6.5 1008 2 T18508
129 80 6.5 1231 2 S70553
130 80 6.5 1388 2 T38720
131 80 6.5 1902 2 S06997
132 79.5 6.4 156 2 A0817
133 79.5 6.4 243 2 H71082
134 79.5 6.4 344 2 B11183
135 79.5 6.4 358 2 G84550
136 79.5 6.4 532 2 C97228
137 79.5 6.4 556 2 C72204
138 79.5 6.4 637 2 S36523
139 79.5 6.4 677 2 D82870
140 79.5 6.4 1211 2 D64702
141 79.5 6.4 1392 2 A43336
142 79.5 6.4 2269 2 T18472
143 79.5 6.4 2894 2 C84474
144 79 6.4 348 2 S96997
145 79 6.4 368 2 A82148
146 79 6.4 378 2 F64446
147 79 6.4 419 2 H81667
148 79 6.4 426 2 B97126
149 79 6.4 628 2 A23393
150 79 6.4 660 2 S70904
151 79 6.4 745 2 D82568
152 79 6.4 788 2 A71076
153 79 6.4 1104 2 A60999
154 79 6.4 1131 2 T19442
155 79 6.4 1902 2 B45764
156 79 6.4 2183 2 T42764
157 79 6.4 4981 2 T18489
158 78.5 6.3 259 2 B82348
159 78.5 6.3 318 2 T38919
160 78.5 6.3 627 2 G37975
161 78.5 6.3 722 2 E71403
162 78.5 6.3 781 2 T36143
163 78.5 6.3 836 2 A90540
164 78.5 6.3 998 2 I41078
165 78 6.3 416 2 A11760
166 78 6.3 476 2 G50512
167 78 6.3 626 2 E95250
168 78 6.3 669 2 T05212
169 78 6.3 681 2 F69295
170 78 6.3 692 2 B64381
171 78 6.3 993 2 A81905
172 78 6.3 1091 2 A81380
173 78 6.3 2013 2 C71610
174 77.5 6.3 241 2 B98888
175 77.5 6.3 252 2 E95884

hypothetical prote
cyclic beta 1-2 gl
hypothetical prote
hypothetical prote
probable carboxyl-
DNA-directed RNA p
alpha-amylose (EC
beta-fructofuranos
diphosphate-fructo
hypothetical prote
collagenase - Clos
hypothetical prote
surface antigen sp
Metalloproteinase II
serine/threonine-s
transposase (O6) B
hypothetical prote
hypothetical prote
type II restrictio
integrin alpha-1 c
restin - human
hypothetical prote
hypothetical prote
porin - common ice
hypothetical prote
chromosome-associ
chromodomain helic
lactocepin (EC 3.4
bacterioferritin c
hypothetical prote
copper ABC transpo
hypothetical prote
probable peptidase A
alpha-amylose - Th
EI protein - human
DNA topoisomerase
DNA polymerase III
microtubule-vesicli
hypothetical prote
hypothetical prote
uncharacterized co
chorismate synthas
transcription term
cystathionine beta
hypothetical prote
transferrin-bindin
conserved hypotet
hypothetical prote
alpha-amylose (EC
hypothetical prote
lactocepin (EC 3.4
coagulation factor
hypothetical prote
probable lipopolys
conserved hypotet
hypothetical prote
hypothetical prote
probable secreted
outer-membrane fim
hemolysin - Escher
P60-like (mycoplas
glycosyl hydrolase
hypothetical prote
acetyl-CoA synthet
hypothetical prote
outer membrane sec
glycosidase homolo
probable membrane
hypothetical prote
hypothetical prote

176 77.5 6.3 361 2 E86692
177 77.5 6.3 372 2 G96933
178 77.5 6.3 419 1 C53312
179 77.5 6.3 429 2 A25145
180 77.5 6.3 467 2 G69849
181 77.5 6.3 522 2 D96913
182 77.5 6.3 547 2 S49815
183 77.5 6.3 554 2 S41526
184 77.5 6.3 581 2 T51580
185 77.5 6.3 590 2 H70130
186 77.5 6.3 609 2 T32302
187 77.5 6.3 707 2 S78538
188 77.5 6.3 709 2 A41976
189 77.5 6.3 817 2 F86742
190 77.5 6.3 1269 2 A90267
191 77.5 6.3 1325 1 S73723
192 77.5 6.3 3206 1 GNVSPV
193 77 6.2 421 2 A11112
194 77 6.2 425 2 T43772
195 77 6.2 500 2 B43577
196 77 6.2 620 2 E90575
197 77 6.2 646 2 H95155
198 77 6.2 797 2 D71621
199 77 6.2 876 2 A89944
200 77 6.2 893 2 S64926

ALIGNMENTS

RESULT 1

A28179
enterotoxin E precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28179
R:Couch, J.L.; Soltis, M.T.; Betley, M.J.
J. Bacteriol. 170, 2954-2960, 1988
A:Title: Cloning and nucleotide sequence of the type E staphylococcal enterotoxin gene.
A:Reference number: A28179; MUID:88257005; PMID:3384800
A:Accession: A28179
A:Molecule type: DNA
A:Residues: 1-257 <COU>
A:Cross-references: UNIPROT:P12993; GB:M21319; NID:g153001; PIDN:AAA26617.1; PID:g153002
C:Superfamily: enterotoxin B

Query Match 100.0%; Score 1238; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. NO. 1.8e-93; Indels 0; Gaps 0;
Matches 233; Conservative 0; Mismatches 0;

QY 1 SEKSEINEKDLRKKSLQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFPTG 60
Db 25 SEKSEINEKDLRKKSLQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFPTG 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDYGYAGYQACAGTTPNKACMYGGVTLHDNNRLT 120
Db 85 HPWYNDLLVDLGSKDATNKYKGVLDYGYAGYQACAGTTPNKACMYGGVTLHDNNRLT 144
QY 121 EEKVPINLWIDGQTTVPIDKVTSKVETVQBLDQARHYLHGKFGLYNSDSFGGKVQ 180
Db 145 EEKVPINLWIDGQTTVPIDKVTSKVETVQBLDQARHYLHGKFGLYNSDSFGGKVQ 204
QY 181 RGLVFFHSSEGSTVSVDLFDQAQGYPTDLRIYRDNKTINSENHLDLYLTT 233
Db 205 RGLVFFHSSEGSTVSVDLFDQAQGYPTDLRIYRDNKTINSENHLDLYLTT 257

RESULT 2

A28664
enterotoxin A precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C:Accession: A28664; A29566

R:Betley, M.J.; Mekalanos, J.J.
J. Bacteriol. 170, 34-41, 1988
A:Title: Nucleotide sequence of the type A staphylococcal enterotoxin gene.
A:Reference number: A28664; MUID:88086892; PMID:3335483
A:Accession: A28664
A:Molecule type: DNA
A:Residues: 1-257 <BET>
A:Cross-references: UNIPROT:P13163; GB:M18970; NID:g153120; PIDN:AAA26681.1; PID:g153121
A:Experimental source: strain FR1337
R:Huang, I.Y.; Hughes, J.L.; Bergdoll, M.S.; Schantz, E.J.
J. Biol. Chem. 262, 7006-7013, 1987
A:Title: Complete amino acid sequence of staphylococcal enterotoxin A.
A:Reference number: A29566; MUID:87222293; PMID:3584106
A:Accession: A29566
A:Molecule type: protein
A:Residues: 25-241, 'S', 243-257 <HUA>
C:Genetics:
A:Gene: entA
C:Superfamily: enterotoxin B

Query Match 82.6%; Score 1023; DB 2; Length 257;
Best Local Similarity 82.0%; Pred. No. 5.9e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 84

QY 61 HPWYNDLLVLDGSKDNTNKGKVDLYGAYYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 85 HSWYNDLLVDFDSKDVIYDKYKGVLDLYGAYYGYQCAGTTPNKTCMYGGVTLHDNNRLT 144

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 145 BEKKVPINLWIDGKQNTVPLGVTKNKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 204

QY 181 RGLIVFHSSEGSTVSYDLFDAQGGQVPTLLRIYRDNKNTINSENHLHIDLYLYT 233
DB 205 RGLIVFHTSTPEPSVNDLFGAQQGYNTLLRIYRDNKNTINSENHWIIDIYLYTS 257

RESULT 3
C89984
enterotoxin P [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89984
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89984
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99SU3; GB:BA000018; PIDN:BA043036.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: sep
C:Superfamily: enterotoxin B

Query Match 80.3%; Score 994; DB 2; Length 260;
Best Local Similarity 79.0%; Pred. No. 1.4e-73;
Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 28 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 87

QY 61 HPWYNDLLVLDGSKDNTNKGKVDLYGAYYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120

DB 88 HQWYNDLLVLDGSKDNTNKGKVDLYGAYYGYQCAGTTPNKTCMYGGVTLHDNNRLT 147
QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 148 BEKKVPINLWIDGKQNTVPLGVTKNKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 207

QY 181 RGLIVFHSSEGSTVSYDLFDAQGGQVPTLLRIYRDNKNTINSENHLHIDLYLYT 233
DB 208 RGLIEFHPSSGSDSVGYDLFGAQQGYPTQLRIYRDNKNTIKSNMHIYLYT 260

RESULT 4
A33953
enterotoxin D precursor - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 09-Jul-2004
C:Accession: A33953
R:Bayles, K.W.; Iandolo, J.J.
J. Bacteriol. 171, 4799-4806, 1989
A:Title: Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin I
A:Reference number: A33953; MUID:89359112; PMID:2549000
A:Accession: A33953
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <BAY>
A:Cross-references: UNIPROT:P20723; GB:M28521; NID:g1492109; PIDN:AAB06195.1; PID:g758699
C:Superfamily: enterotoxin B

Query Match 53.6%; Score 663; DB 2; Length 258;
Best Local Similarity 54.5%; Pred. No. 1.2e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 26 NENIDSVKEKELKSELSSTALNNKHSYADKNPIGENKSTGDOFLENTLLYKFFTD 85

QY 61 HPWYNDLLVLDGSKDNTNKGKVDLYGAYYGYQCAGTTPNKTCMYGGVTLHDNNRLT 120
DB 86 LINFEDLLINFNSKEMAHQFKSKVDVPIRYSINCYGGEIDRTACTYGGVTPHEGNLKL 145

QY 121 BEKKVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 180
DB 146 ERKKIPINLWINGVQKESVSLDKVQTDKKNVTVOELDLQARHYLHGKFLYNSDSFGKVKQ 205

QY 181 RGLIVFHSSEGSTVSYDLFDAQGGQVPTLLRIYRDNKNTINSENHLHIDLYLY 231
DB 206 RKIEFDSDSGSKSVYDLFDVKGDFPEKQLRIYSDNKTLSLHIDLYLY 256

RESULT 5
H89968
enterotoxin SeN [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, M.; Mizutani, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:Q9EZM4; GB:BA000018; PIDN:gl3701618; PIDN:BA042911.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: sen
C:Superfamily: enterotoxin B

Query Match 37.3%; Score 461.5; DB 2; Length 258;

Best Local Similarity 41.2%; Pred. No. 3.1e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;
QY 6 EINEKRLRKSELQARNLSNLRLQIYYNEKAIT-----ENKESDDQFLENTLLFKGFFTG 60
Db 32 EVDKKDLKKSLDSSKLFNITS--YYTD--ITWQDESNNKISTDQLLNNTIILNKIDIS 87
QY 61 HPWYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLT 120
Db 88 VLKTSLSKAVFNSSDLANQPKGNIDYGLFGNKCVELTEKTSCLYGGVTIHDGQOLD 147
QY 121 BEKKVPINLWIDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFGGKVQ 180
Db 148 BEKVGIVNVFQGVQOEGFV--IKTKKAKVTQVELDTKVRFKLENLYKIYNKDT--GNIQ 203
QY 181 RGLVPHS--SEGSTVSVYDLFDAQGYDPTLLRIYRDNKTINSENHLIDLVL 231
Db 204 KGCIFFHSHNHQDSFYDLYNVKSGVGAEPFQFYSDNRNTVSSNYHIDVELY 256
RESULT 6
E89969
enterotoxin SeO [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-260 <KUR>
A:Cross-references: UNIPROT:Q99T46; GB:BA000018; PID:g13701623; PIDN:BAB42916.1; GSPDB:G89969
A:Experimental source: strain N315
C:Genetics:
A:Gene: sei
C:Superfamily: enterotoxin B
Query Match 31.3%; Score 387.5; DB 2; Length 260;
Best Local Similarity 39.9%; Pred. No. 3.3e-24;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;
QY 8 NEKD-----LRKSELQARNLSNLRLQIYYNE-----KAITENKESDDQFLENTLLFKGFF 58
Db 29 NEEDPKIESLCKSSVDPIALHNINDYINNRFTTVKSIIVTTE---KFLDFDILLFKSI- 84
QY 59 TGHPW-----YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGV 111
Db 85 ---NWLDSIAEFKDLKVEFSSAISKEFLGKTVDIYGVYKACHGHBQVDTACTYGGV 141
QY 112 TLHDNNRLTEKKVPINLWIDGQTTVPIDKVKTSKKEVTQVELDQARHYLHGKFGLYN 171
Db 142 TPHENNKLSPEKNIGVAVYKDNVNVNTFI--VTTDKKVTQAQELDKVTKLNAYKLY- 198
QY 172 SDSFGGKVQRLGIYVPHSSEGSTVS--YDLFDAQGYDPTLLRIYRDNKTINSENHLIDL 229
Db 199 -DRMTSDVQKGIKPHSHSEHKESFYDLYFKGNLPDQYLIQIYNDNKTIDSIDYIDVY 257
QY 230 LYT 232
Db 258 LFT 260
RESULT 7
E89969
extracellular enterotoxin type I precursor [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: E89969

R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: E89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-242 <KUR>
A:Cross-references: UNIPROT:O85383; GB:BA000018; PID:g13701621; PIDN:BAB42914.1; GSPDB:G89969
A:Experimental source: strain N315
C:Genetics:
A:Gene: sei
C:Superfamily: enterotoxin B
Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 2.5e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;
QY 23 LSNLRQIY---YVNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLLVDLGSKDATN 78
Db 30 VGNLRFYTKHDYIDLKGVTDKNLPANQLE-----FSTG---TNDLISESNWDEIS 79
QY 79 KYGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGQTTV 138
Db 80 KFKGKGLDIFGIDVNGPC-----KSKVYGGATL-SGQYLSNARKIPINLWVNGKHKTI 132
QY 139 PIDKVKTSKKEVTQVELDQARHYLHGKFGLYNSDSFG-GK-----VQRLIVP 186
Db 133 STDKIATNKKLVTAQELDVKLRLRYLQBEYNIYGHNTGKGKEYGYKSKFYSGFNKGKVL 192
QY 187 HSSGTSVSVYDLFDAQGYDPTLLRIYRDNKTINSENHLIDL 228
Db 193 HLNNEKSFSDLYFTGGGLPVSPFKIYEDNKIIESEKFHLDV 234
RESULT 8
G89991
extracellular enterotoxin L [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89991
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.; Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; PMID:21311952; PMID:11418146
A:Accession: G89991
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-240 <KUR>
A:Cross-references: UNIPROT:Q9F0L7; GB:BA000019; PID:g13701803; PIDN:BAB43096.1; GSPDB:G89991
A:Experimental source: strain N315
C:Genetics:
A:Gene: sei
C:Superfamily: enterotoxin B
Query Match 27.2%; Score 337; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 3.9e-20;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;
QY 25 NLROIY---YVNEKAITENKESDDQFLENTLLFKGFFTGHPWYND--LLVDLGSKDATNK 79
Db 32 NLRNFYTKYEYVNLKVNKDNKNSPESHLE-----YSYKNDTLAYAFDEHYITSD 80
QY 80 YGKKVDLYGAYGYQCAGGTPNKTACMYGGVTLHDNNRLTEKKVPINLWIDGQTTVP 139
Db 81 LKGNVDVFGISYKY---GSNSRT--IYGGVTKAENNKLDSPRIIPINLIINGKHQVTV 134
QY 140 IDKVKTSKKEVTQVELDQARHYLHGKFGLY-----NSDSFGGKVQRLIVP 187

R;Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3511-3517, 1970
A;Title: The primary structure of staphylococcal enterotoxin B. II. Isolation, compositional analysis, and properties of the toxin.
A;Reference number: A92064; PMID:71007901; PMID:5470820
A;Contents: annotation; chymotryptic peptides
R;Huang, I.Y.; Bergdoll, M.S.
J. Biol. Chem. 245, 3493-3510, 1970
A;Title: The primary structure of staphylococcal enterotoxin B. I. Isolation, composition, and properties of the toxin.
A;Reference number: A92063; PMID:71007900; PMID:5470819
A;Contents: annotation; tryptic peptides
R;Schantz, E.J.; Roesser, W.G.; Wagman, J.; Spero, L.; Dunnery, D.A.; Bergdoll, M.S. Biochemistry 4, 1011-1016, 1965
A;Title: Purification of staphylococcal enterotoxin B.
A;Reference number: A90548; PMID:56035792; PMID:4953912
A;Contents: annotation; biological source of protein
R;Alakhov, V.Y.; Klinisky, E.Y.; Kolosov, M.I.; Maurer-Poggy, I.; Moskaleva, E.Y.; Svishniuk, J. J. Biochem. 209, 823-828, 1992
A;Title: Identification of functionally active fragments of staphylococcal enterotoxin B. A;Reference number: S27240; PMID:93049338; PMID:1425690
A;Accession: S27240
A;Molecule type: protein
A;Residues: 28-42;128-148 <ALA>
C;Superfamily: enterotoxin B
C;Keywords: enterotoxin; extracellular protein; toxin
F;1-27/Domain: signal sequence #status predicted <SIG>
F;28-266/Product: enterotoxin B #status experimental <MAT>
F;120-140/Disulfide bonds: #status experimental

Query Match 24.3%; Score 300.5; DB 1; Length 266;
Best Local Similarity 33.6%; Pred. No. 4.2e-17;
Matches 82; Conservative 47; Mismatches 96; Indels 19; Gaps 8;

Qy 1 SEKSEINEKDLRKKSLEQNALSNLRQIYYNEKAITENKESDDQFLNTLLFKGFPFG 60
Db :
27 AESQDPKPDELHKSRP-TGLMENMKVLYDNNHVSAI-NVKSIDQFLYFDLIYSIKDTK 84
Qy :
61 HPWYNLDLVLGSKDAFNKYGGKKVDLYGAYGYQC-----AGTGNPKTA CMYG 110
Db :
85 LGNYDNVRVEFNKLADKYDKVDFVGANYYYCYFSKKTNDINSHQTDRKTKCMYGG 144
Qy :
111 VTLDHNRLNTEKKVPINLMDIGKQTTVPIDKVTSKKEVTVQELDLQARHYLVHGKFGLY 170
Db :
145 VTEHNGNLQDKYSITVRVFEDKG-NLLSFP-VQTNKKKVTAQELDYLTRHYLVVNKKCLY 202
Qy :
171 NSDSFGCKVQRGLIVFHSSSEGTSVYDLFDAOGQYPD--TLIRIYRDNKNTINSENLIIDL 228
203 EFNN--SPYETGYIKFIENENS-FWYDMNPAGKDFQSKYLMTYNDKNWDSDKDVIEV 259

Db 260 YLTT 263

RESULT 11

S29659
exotoxin type A precursor (allele 1) - Streptococcus pyogenes phase T12
N;Alternate names: erythrogenic toxin; scarlet fever toxin
C;Species: Streptococcus pyogenes phase T12
C;Date: 10-Sep-1999 #sequence revision 10-Sep-1999 #text change 10-Sep-1999
C;Accession: S29659; S18782; S18784; S18785; S18791; S18796; S18797; S18800
R;Weeks, C.R.; Ferretti, J.J.
Infect. Immun. 52, 144-150, 1986

A;Title: Nucleotide sequence of the type A streptococcal exotoxin (erythrogenic toxin) 96
A;Reference number: S29659; MUID:86166804; PMID:3514452
A;Accession: S29659
A;Molecule type: DNA
A;Residues: 1-251 <WEE>
A;Cross-references: GB:U40453; EMBL:M19350; NID:gl877426; PIDN:AAC48668.1; PID:gl877430
R;Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
J. Exp. Med. 174, 1271-1274, 1991

A;Title: Characterization and clonal distribution of four alleles of the speA gene encoding
A;Reference number: S18782; MUID:92044323; PMID:1940804
A;Accession: S18782

A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61560; NID:G47287; PIDN:CAA43758.1; PID:G47288
A:Experimental source: Streptococcus pyogenes strain MGAS156 isolate Nebraska unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18784
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61556; NID:G47291; PIDN:CAA43754.1; PID:G47292
A:Experimental source: Streptococcus pyogenes strain MGAS165 isolate Minnesota unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18785
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61559; NID:G47293; PIDN:CAA43757.1; PID:G47294
A:Experimental source: Streptococcus pyogenes strain MGAS167 isolate Texas unassigned ph
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18791
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61555; NID:G47309; PIDN:CAA43753.1; PID:G47310
A:Experimental source: Streptococcus pyogenes strain MGAS327 isolate Arizona unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18796
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61557; NID:G47319; PIDN:CAA43755.1; PID:G47320
A:Experimental source: Streptococcus pyogenes strain MGAS493 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18797
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-244 <NE>
A:Cross-references: EMBL:X61558; NID:G47321; PIDN:CAA43756.1; PID:G47322
A:Experimental source: Streptococcus pyogenes strain MGAS494 isolate France unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
A:Accession: S18800
A;Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 9-228 <NE>
A:Cross-references: EMBL:X61554; NID:G47327; PIDN:CAA43752.1; PID:G47328
A:Experimental source: Streptococcus pyogenes strain MGAS500 isolate New Zealand unassigned
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, September 1991
C:Genetics:
A:Gene: speA; speA
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-251/Product: exotoxin type A #status predicted <MAT>

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best Local Similarity 34.2%; Pred. No. 9.9e-17;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

Qy 4 SEEINEKDLRKSEIQNAL-SNLRIQYY-YNEKAIT-ENKESDDQFLENTLLFKGFTG 60
Db 25 SQEVPAAQDDPSQLSRSLVKNLQNIYFLYEGDPVTHENVKSVQDLLSHDLIYN--VS 81

Qy 61 HPWYNDLLVDSKDATNKYKKVDLYGAYGYQC-AGGTPNKTCACMYGGVTLHDNNRL 119
Db 82 GPNYDKLKTSLKQSMATLFFKDKNVDIYGVVEYHLCYLCNAERSACTYGGVTNHEGNH 141

Qy 120 TEEKKVPINLWDGQTTVPIDKVKTSKKEVTQELDLQARHYLHGKFGLYNSDSFGGKV 179
Db 142 EIPKIVVKNVSDIGIQ-SLSFD-ISTNKKVTAQELDYKVRKYLFDNKQLYNGP--SKY 197

Qy 180 ORGLIVFHSSEGSTVSYDLFD----AQGQYPTLLRIYRDKNKTINSENHLIDL 232

Db 198 ETGIKPIPKNKESFWDFPFPEFTQSKY----LMIYKDNETLDSNTSQIEVLTT 250

RESULT 12
S11885
enterotoxin C3 - Staphylococcus aureus
C:Species: Staphylococcus aureus
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
A:Accession: S11885
R:Howde, C.J.; Hackett, S.P.; Bohach, G.A.
Mol. Gen. Genet. 220, 329-333, 1990
A:Title: Nucleotide sequence of the staphylococcal enterotoxin C3 gene: sequence compari
A:Reference number: S11885; MUID:90220508; PMID:2325627
A:Accession: S11885
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <HOV>
A:Cross-references: UNIPROT:P23313; GB:X51661; NID:G46570; PIDN:CAA35972.1; PID:G46571
C:Superfamily: enterotoxin B

Query Match 23.1%; Score 285.5; DB 2; Length 266;
Best Local Similarity 32.1%; Pred. No. 7e-16;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

Qy 11 DLRKSEIQNALSNLRQIYYNEKAITENK-ESDDQFLENTLLFKGFTGHPWYNDLLV 69
Db 37 DLKSSSEF-TGTGMNKK--LYDDHYVSATKVKSVDKFLAHDLIYVNSDKKLKNYDKVKT 93

Qy 70 DLGSKDATNKYKKVDLYGAYGYQC-----AGGTPNKTCACMYGGVTLHDNNRLTEE 122
Db 94 ELLNEDLAKYKDEWVDVYGSNNYVNCYFSSKDNVGVKVTGKTCMYGGITKHGHNHFDNG 153

Qy 123 --KKVPINLWDGQTTVPIDKVKTSKKEVTQELDLQARHYLHGKFGLYNSDSFGGKVQ 180
Db 154 NLQNVLRVY-ENKRTISFE-VTDKKSVAQELDKARNFLNKKKLYEFNS--SPYE 209

Qy 181 RGLIVFHSSEGSTVSYDLFDAQGQYD--TLLRIYRDKNKTINSENHLIDL 232
Db 210 TGIYKFIENNGNTFWYDMPAPGDKFQSKYLMYNDNKTVDTSKSVKIEVHLT 263

RESULT 13
A60114
enterotoxin C-2 precursor - Staphylococcus aureus
N:Alternate names: enterotoxin C-3 precursor
C:Species: Staphylococcus aureus
C:Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C:Accession: A60114; B60114; A33866
R:Bohach, G.A.; Schlievert, P.M.
Infect. Immun. 57, 2249-2252, 1989
A:Title: Conservation of the biologically active portions of staphylococcal enterotoxins
A:Reference number: A60114; MUID:89277549; PMID:2543637
A:Accession: A60114
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-266 <BOH>
A:Cross-references: UNIPROT:P34071
A:Accession: B60114
A:Molecule type: protein
A:Residues: 28-66 <BOH2>
R:Couch, J.L.; Betley, M.J.
J. Bacteriol. 171, 4507-4510, 1989
A:Title: Nucleotide sequence of the type C-3 staphylococcal enterotoxin gene suggests the
A:Reference number: A33866; MUID:89327174; PMID:2473979
A:Accession: A33866
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-266 <COU>
A:Cross-references: GB:M28364; NID:g153003; PIDN:AAA26624.1; PID:g153004
C:Genetics:
A:Gene: entC2
C:Superfamily: enterotoxin B
F:1-27/Domain: signal sequence #status predicted <SIG>

Query Match	22.0%;	Score 272.5;	DB 2;	Length 236;
Best Local Similarity	33.3%;	Pred. No. 6.9e-15;		

RESULT 18
extracellular enterotoxin type G precursor [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89968
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89968
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-258 <KUR>
A:Cross-references: UNIPROT:O85382; GB:BA000018; PID:gl3701617; PIDN:BAB42910.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: seg
C:Superfamily: enterotoxin B

Query Match 20.6%; Score 255.5; DB 2; Length 258;
Best Local Similarity 29.1%; Pred. No. 1.9e-13;
Matches 71; Conservative 49; Mismatches 83; Indels 41; Gaps 11;

QY 11 DLKKESELQNR--ALSNLRQIYY--YNEKAITENKESDDQFLENTLLFKGFFTGHPWYN 65
DB 33 ELNKVSDYKNNKGTGWNVNLTPSPVEGRVINSR----QFLSHDLIFP---IEVKSYN 85
QY 66 DLLVLDGSKDATNKYKGGKVDLYGAYGYQCA-----GGTPNKATCMYGGVTL 113
DB 86 EVKTELENTLANNYKDKKVDIFGVFYTCIIPKSEPDINQNFSG-----CMYGGTLF 140
QY 114 H--DNNLTTEKKVPINLMDGKQITVPIDKVKTSKKEVTVQELDLQARHYLHGRFGLN 171
DB 141 NSENER---DKLITVQVTDNRSLG--FTITTKNMVTVIQLDYKARHLLTKKKGLYE 195
QY 172 SPSFGKVGRLIVFHSRSGTSVSYDLFDAQGYDPT---LLRIYRDNTKNTINSENHIDL 228
DB 196 FD--GSAPFSGYIKFKTEKNTSFWDLPFKKELVPPVVKFLNIYCDNKVDSKSKMEV 253
QY 229 YLYT 232
DB 254 FLNT 257

RESULT 19
A26152
streptococcal pyrogenic exotoxin type A precursor - Streptococcus sp.
N:Alternate names: scarlet fever toxin; SPE type A (speA)
C:Species: Streptococcus sp.
C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C:Accession: A26152
R:Johnson, L.P.; L'italien, J.J.; Schlievert, P.M.
Mol. Gen. Genet. 203, 354-356, 1986
A:Title: Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is related to Sta
A:Reference number: A26152; MUID:86284313; PMID:3526093
A:Accession: A26152
A:Molecule type: DNA
A:Residues: 1-250 <JOH>
A:Cross-references: UNIPROT:P08095
C:Superfamily: enterotoxin B
C:Keywords: exotoxin

Query Match 19.8%; Score 245; DB 1; Length 250;
Best Local Similarity 30.7%; Pred. No. 1.3e-12;
Matches 70; Conservative 42; Mismatches 94; Indels 22; Gaps 9;

QY 14 KKESELQNRALSNLRQIYYNEKA--IT-ENKESDDQFLENTLLFKGFFTGHPWYNLLVD 70
DB 35 KPSQLQSRNLVTKYIFFMVTVLTHENVKSDVQLLSDHLLYN---VSGPNYDKLKTE 91

QY 71 LGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKATCMYGGVTLHNNRLTEKKVPINL 129
DB 92 LKNOEMATFLDKDNVDIYGVYIHLCYLCENAESACLYGGVTNHEGHLEIPKXIVVVKV 151
QY 130 WIDGKQT--TVPIDKVKTSKKEVTVQELDLQARHYLHGRFGLYNSDSFGKVGQRLIVFHS 188
DB 152 SIDGLOSLSPDIEQIKNG---NCSRISTYVRKYLTDNKLQLYTNGP--SKYETGYIKFTP 205
QY 189 SEGSTVSVDLPD---AGQVPDPTLLRIYRDNTKNTINSENHIDLILYLT 232
DB 206 KNKESFWDFPEPEFTQSKY----LMIYKDNETLDSNTSQIEVYLT 249

RESULT 20
A89942
hypothetical protein SA1430 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89942
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89759; MUID:21311952; PMID:11418146
A:Accession: A89942
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-157 <KUR>
A:Cross-references: UNIPROT:Q99TP7; GB:BA000018; PID:gl3701400; PIDN:BAB42694.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1430

Query Match 16.2%; Score 201; DB 2; Length 157;
Best Local Similarity 35.6%; Pred. No. 2.7e-09;
Matches 42; Conservative 21; Mismatches 53; Indels 2; Gaps 2;

QY 1 SEKSEINEKDLRKSELRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
DB 42 TNSASAIKESYDLHKKSKFDSKLSNAK--MSFINPTQL--ENKNTNDRLLKHLDFHDMFVN 99
QY 61 HPWYNDLLVLDGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKATCMYGGVTLHNNR 118
DB 100 VASKKDFKVFENEALSKKFINKINDIYAGSYSECHGGATNKTQCSGGVTLSDNNK 157

RESULT 21
A89969
enterotoxin YENT2 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-136 <KUR>
A:Cross-references: UNIPROT:Q99T49; GB:BA000018; PID:gl3701619; PIDN:BAB42912.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: yent2

Query Match 15.9%; Score 197; DB 2; Length 136;
Best Local Similarity 34.1%; Pred. No. 4.8e-09;
Matches 46; Conservative 28; Mismatches 51; Indels 10; Gaps 5;

QY 103 KTACMYGGVTLHNNRLTEKKV--PINLW----DGQITVPIDKVKTSKKEVTVQELDL 157

Db 2 KKTWGGVTEHDGNOIDKNNSTDNHILKVVYENRNSLSFD-IPNKKKNITAEIDY 60
Qy 158 QARHLYHCKFGLYNSDSFGGKVQRLIVFHSSEGSTVSYDLFDAQQ--YPTLLRIYRD 215
Db 61 KVRNLLKHKNLYEFNS--SPYETGYIKFIEGSGHSPWYDLMPBSGKKFYPTKYLIIYND 118
Qy 216 NKTINSENHLIDLVL 230
Db 119 NKTVESKSINVEVHL 133
RESULT 22
A30509
exotoxin C precursor - Streptococcus pyogenes
C:Species: Streptococcus pyogenes
C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C:Accession: A30509
R:Goshorn, S.C.; Schlievert, P.M.
Infect. Immun. 56, 2518-2520, 1988
A:Title: Nucleotide sequence of streptococcal pyrogenic exotoxin type C.
A:Reference number: A30509; MUID:88314303; PMID:3045005
A:Accession: A30509
A:Molecule type: DNA
A:Residues: 1-235 <GOS>
A:Cross-references: UNIPROT:P13380; GB:M35514; NID:g153820; PIDN:AAA27017.1; PID:g153821
C:Superfamily: enterotoxin B
C:Keywords: exotoxin
Query Match 14.8%; Score 183.5; DB 2; Length 235;
Best Local Similarity 25.8%; Pred. No. 1.2e-07;
Matches 61; Conservative 37; Mismatches 73; Indels 65; Gaps 11;
Qy 47 FLENTLFLKGFFTGH-----PW-YNDLLVDLGSKDA-----TNK 79
Db 11 FIITVILISTFTYHQSDSKDISNVKSDLLAYVITPYDKDCRVNFSFTTHLINIDTQK 70
Qy 80 YKKG-----KVDLYGAVYGVQCAGGTPNKTACMYGGVTLHDNNRL 119
Db 71 YRGKDYISSEMSYASQKFRDDHVDVFGLYILNSHTG-----EYIGGITPAQNNKV 125
Qy 120 TEKKVPINLMDGKQTTPIDKVKTSKKEVTVOELDLQARHLYHCKFGLYNSDS--FGG 177
Db 126 NH--KLLGNLFISGESQQNNKNIILEKDIVTFQEIDPKIRKLYMDNVIKYDATSPYVSG 183
Qy 178 KVQRLIVFHSSEGSTVSYDLFDA--QQYPTLLRIYRDNKTINSENL-HIDLVL 230
Db 184 RIEIG-----TKDGKHEQIDLDFSPNEGTRSDIFAK-YKDNRIINMKNFSDIYL 233
RESULT 23
H89941
hypothetical protein SA1429 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: H89941
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: H89941
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <KUR>
A:Cross-references: UNIPROT:Q99TP8; GB:BA0000018; PID:g13701399; PIDN:BAB42693.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1429
Query Match 11.6%; Score 144; DB 2; Length 62;
Best Local Similarity 39.3%; Pred. No. 3.7e-05;

Matches 22; Conservative 16; Mismatches 18; Indels 0; Gaps 0;
Qy 176 GKGVQRLIVFHSSEGSTVSYDLFDAQQYPTLLRIYRDNKTINSENHLIDLVL 231
Db 5 GGDIVKGVTKVTHNDDEQNVEYDFNLNGEYGEYEVZKMYADNKTINRDKLHLDIYLF 60
RESULT 24
B89969
enterotoxin Yent1 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89969
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89969
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <KUR>
A:Cross-references: UNIPROT:Q99T48; GB:BA0000018; PID:g13701620; PIDN:BAB42913.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: Yent1
Query Match 9.9%; Score 123; DB 2; Length 133;
Best Local Similarity 30.0%; Pred. No. 0.005;
Matches 39; Conservative 25; Mismatches 38; Indels 28; Gaps 8;
Qy 3 KSEINEKDLRKKSELQORNALNLRIQIYYNEKAITE-NKESDDQFLENTLLFKGFFTGH 61
Db 25 KPEQLN-----KASEP-TGLMDNMR--YLYDDKHVSEINIKSQKFLQDHLFK--INGS 74
Qy 62 PWYNDLLVDLGSKDATNKYKGGKVDLYGAVYGVQCAGGTPNKTACMYGGVTLHDNNRLTE 121
Db 75 ---KILATEFPNKSLSKYKKNVDFLGTNYNQC-----YFSL---DNMELND 117
Qy 122 EKKVPINLMI 131
Db 118 GRLEKRVIV 127
RESULT 25
F89807
exotoxin 13 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C>Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: F89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguchi, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: F89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: UNIPROT:Q99WH4; GB:BA0000018; PID:g13700319; PIDN:BAB41617.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set13
C:Superfamily: toxic shock syndrome toxin
Query Match 9.1%; Score 113; DB 2; Length 232;
Best Local Similarity 24.5%; Pred. No. 0.065;
Matches 59; Conservative 29; Mismatches 79; Indels 74; Gaps 12;
Qy 17 ELQRNALNLRIQIYYNEKAITEN--KESDDQFLENTL-----LFKGFFTGHFWYNDL 67

Db 36 ETQRKYINMLHQYYSEBSFESTNISVKSSEDYVGNVLFNQRNRTFKVFLLG----- 88
Qy 68 LVDLGSKDATNKYKGGK-----VDLYGAYGYQCAGGTGPNKTACMYGGVTLHDN 116
Db 89 -----DDKNKYKEKTHGLDVFAPVELIDIKGGI--YVGGITKKVRSVFGFV---S 135
Qy 117 NRLTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLYNSDSFG 176
Db 136 NPSLQVKKV-----DAKHGFSINELFFTKQEVSLKELDFKIRKMLVEKRYLYK----- 184
Qy 177 GKVQGLIVFHSSE-----GSTVSYD-LFDAQGYQPDTLRLIYRDNKTINSENHLID 227
Db 185 GASDGRIVNMKDEKKYVLDLSEKLSFDRMFDVM-----DSKQI--KNIEVN 230
Qy 228 L 228
Db 231 L 231

RESULT 26
XCSAS1
N:Alternate names: TSST-1
C:Species: Staphylococcus aureus
C:Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 09-Jul-2004
C:Accession: A24606; B24606
R:Blomster-Hautamaa, D.A.; Kreiswirth, B.N.; Kornblum, J.S.; Novick, R.P.; Schlievert, H.
J. Biol. Chem. 261, 15783-15786, 1986
A:Title: The nucleotide and partial amino acid sequence of toxic shock syndrome toxin-1.
A:Reference number: A24606; MUID:87057222; PMID:3782090
A:Accession: A24606
A:Molecule type: DNA
A:Residues: 1-234 <BLO>
A:Cross-references: UNIPROT:P06886; GB:J02615; NID:gi513122; PID:AAA26682.1; PID:gi513123
A:Accession: B24606
A:Molecule type: protein
A:Residues: 41-106;199-224 <BLO2>
A:Note: The authors translated the codon ACT for residue 20 as Ile and GGG for residue 1
C:Superfamily: toxic shock syndrome toxin
C:Keywords: toxic shock syndrome; toxin
F:1-40/Domain: signal sequence #status predicted <SIG>
F:41-234/Product: toxin shock syndrome toxin-1 #status experimental <MAT>

Query Match 8.7%; Score 107.5; DB 1; Length 234;
Best Local Similarity 23.0%; Pred. No. 0.19;
Matches 53; Conservative 35; Mismatches 69; Indels 73; Gaps 12;

Qy 11 DLKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTGHPWYNDLLVD 70
Db 58 DFTFTNSEVLDNSLGSMR-----IKNTDGSII--SLIIFPS-----PYSPAF-- 97
Qy 71 LGSKDATNKYKGGKVDL-----YGAYGYQCAGGTGPNKTACMYGGVTLHDNR 118
Db 98 -----KGEKVDLNTKTKKSQHTSEGTYIHFGISGVT-----NTEK 133
Qy 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLY-NSDSFG 177
Db 134 LPTPIELPKVKVHGKDSPLKYGP-KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDKTG 192
Qy 178 --KVQGLIVFHSSEGSTVSVDL---FDAQGYQPDTLRLIYRDNKTINSE 222
Db 193 YWKIT-----MNDGSTYQSDLSKKFVNTKPPINI---DEIKTIEAE 232

RESULT 27
B89992
toxic shock syndrome toxin-1 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89992
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89992
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-234 <KUR>
A:Cross-references: UNIPROT:O54462; GB:BA000018; PID:gi13701806; PIDN:BABA3099.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics:
A:Gene: tst
C:Superfamily: toxic shock syndrome toxin

Query Match 8.5%; Score 105.5; DB 2; Length 234;
Best Local Similarity 23.2%; Pred. No. 0.27;
Matches 54; Conservative 35; Mismatches 65; Indels 79; Gaps 13;

Qy 11 DLKKSSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLPKGFTGHPWYNDLLVD 70
Db 58 DFTFTNSEVLDNSLGSMR-----IKNTDGSII--SLIIFPS-----PYSPAF-- 97
Qy 71 LGSKDATNKYKGGKVDL-----YGAYGYQCAGGTGPNKTACMYGGVTLHDNR 118
Db 98 -----KGEKVDLNTKTKKSQHTSEGTYIHFGISGVT-----NTEK 133
Qy 119 LTEKKVPINLWDGKQTTVPIDKVKTSKEVTVQELDLQARHYLHGKFGFLY-NSDS 174
Db 134 LPTPIELPKVKVHGKDSPLKYWP---KFDKKQLAISTLDPEIRHQLTQIHGLYRSSDK 189
Qy 175 FGG--KVQGLIVFHSSEGSTVSVDL---FDAQGYQPDTLRLIYRDNKTINSE 222
Db 190 TGGYWKIT-----MNDGSTYQSDLSKKFVNTKPPINI---DEIKTIEAE 232

RESULT 28
B89807
exotoxin 12 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, R.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-232 <KUR>
A:Cross-references: UNIPROT:Q99WH5; GB:BA000018; PID:gi13700318; PIDN:BABA1616.1; GSPDB:G
C:Experimental source: strain N315
C:Genetics:
A:Gene: set12
C:Superfamily: toxic shock syndrome toxin

Query Match 8.2%; Score 101; DB 2; Length 232;
Best Local Similarity 24.3%; Pred. No. 0.62;
Matches 60; Conservative 33; Mismatches 94; Indels 60; Gaps 11;

Qy 3 KSEENKDLRKKSSELQNALSNLRQIYY---NEKAITENKESDDQFLENTLLPKGFF 58
Db 24 ENQSVNAKGYEK---MNRLYDTNKLHQYSGPSYELTNVSGSQGYDSNVLLF--- 75
Qy 59 TGHFWNDLLDLGSKDATNKYKGGK-----VDLYGAYGYQCAGGTGPNKTACM 107
Db 76 --NQKNQKQFVLLGKD-ENKYKTKTHGLDVFAPVELVDLGRIFS----- 118
Qy 108 YGVTLHDNRNLTTEKKVPINLW---IDGKQTTVPIDKVKTSKEVTVQELDLQARHYLH 164
Db 119 VSGVTKKVKSFSFESLRTP-NLLVKKLIDDKDGSIDEPFFIQKEEYSLKELDFKIRKLLI 177
Qy 165 GKFGLYNSDSFGKQVQRGLIVFHSSEGSTVSVDLFDPAQGYQPDTLRLIYRDNKTINSE-- 222

Db 178 KKYKLYE-----GSADKGRIVNMKNKDKYBIDLSDK-----LDPERMADVINGEQI 224
Qy 223 -NLHIDL 228
Db 225 KNIEVNL 231

RESULT 29
D89807
exotoxin 11 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: D89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: D89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-231 <KUR>
A:Cross-references: UNIPROT:Q99WH6; GB:BA0000018; PID:g13700317; PIDN:BA041615.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set11

Query Match 8.0%; Score 99.5; DB 2; Length 231;
Best Local Similarity 24.0%; Pred. No. 0.82;
Matches 56; Conservative 31; Mismatches 93; Indels 53; Gaps 11;

Qy 2 EKSSEINE-----KDLRKSELQNALSNLR-QIYYN-EKAITENKESDDQFLENTLLFK 55
Db 32 EKQERVQHLVDIKOLYRYSSEFEFSNISKVENYNGSNVRFNQEK-----QNHQLF- 85
Qy 56 GFTGHPWYNDLLVDLGSKDATNKYK---GKVDLYGAYGYQCAGGTPNKTACMGVGV 111
Db 86 -----LLGKD-KDKYKGLQGNVFFVKELI-----DPNGRLSTVGCV 122
Qy 112 TLHNNRLTEKKVPINLWIDGKQTPVPIDKVKTSKKEVTVOELDLQARHYLHGKFGLYN 171
Db 123 TKONKSSETNHLFPVK-VYGGNLDAISIDFSLINKBEVSLKELDFKIRKQLVEKYGLYK 181
Qy 172 SDSFGGKVQGLIVPHSSEGSTVSVDLFDAGQGPDTLLRYRDNKNTINSEN 224
Db 182 -----GTTKYKITINLXDKKEVIDLGDK-----LQPERMGDVILNSKDI 221

RESULT 30
G89807
exotoxin 14 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89807
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:213111952; PMID:11418146
A:Accession: G89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-227 <KUR>
A:Cross-references: UNIPROT:Q99WH3; GB:BA0000018; PID:g13700320; PIDN:BA041618.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set14
C:Superfamily: toxic shock syndrome toxin

Query Match 7.8%; Score 96; DB 2; Length 227;

Best Local Similarity 26.7%; Pred. No. 1.5;
Matches 54; Conservative 28; Mismatches 76; Indels 44; Gaps 9;

Qy 8 NEKDRLK--KSELQNALSNLRQIYYNKAITENKESDDQFLENTLLFKGFTGHPWYN 65
Db 33 NQKSVNKHDXEALYR-----YYTGKTMEMKNISALKHGKNNLRFK--FRGIKIQV 80
Qy 66 DLLVDLGSKDATNKYK-----KKVDLYGAYGYQCAGGT--PNKTACMGVGYTLHDN 116
Db 81 LLPGNDKSKQORSYEGLDVFFVQEKDKHDFY---TVGGVIQNNKTS-----GVVSAPI 133
Qy 117 NRLTEKKVPINLWIDGKQTPVPIDKVKTSKKEVTVOELDLQARHYLHGKGLYNSDSFG 176
Db 134 LNISKEK-----GEDAPVKGPYPYIKKEKITLKELDYKLRKHLIKYGLYKNTISK 184
Qy 177 GKVQGLIVPHSSEGSTVSVDL 198
Db 185 GRVKISL-----KDGSPYNLDDL 201

RESULT 31
G86903
cell shape determining protein [imported] - Lactococcus lactis subsp. lactis (strain IL1;
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: G86903
R;Bolotin, A.; Wincker, P.; Manger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: G86903
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-291 <STO>
A:Cross-references: UNIPROT:Q9CDI9; GB:AS005176; PID:g12725299; PIDN:AAK06329.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: mreC

Query Match 7.6%; Score 94.5; DB 2; Length 291;
Best Local Similarity 20.7%; Pred. No. 2.8;
Matches 48; Conservative 26; Mismatches 67; Indels 91; Gaps 8;

Qy 21 NALSNLRQIYYNKAIT-----ENK-----ESDDQFLENTLLFKGFTTGH----- 61
Db 67 NELSNLMDTYQONQSLKTQLAKSKDDNKLGLSENKELKALKJQETLTDYQTVAANV 126
Qy 62 -----PWYNDLLVDLGSKDATNKYKGGVDLYGAYGYQCAGGTPNKTACMGVGYTLHD 115
Db 127 ITRPSSWNDDTLVIDSGSKD-----GLTTGMVNMANGGV--- 161
Qy 116 NNRLTE-----EKKVPINLWIDGKQTPVPIDKVKTSKKEVTVOELDLQ 158
Db 162 -GRVTQNNKSNKVALSSKGIQNKIPVRIESDGSPIYIGLSSVDSQAEAVVKNIDSQ 220
Qy 159 ARHYLHGKFGLYNSDSFGKQVQGLIVPHSSEGSTVSVDLFDAGQGPDTLL 210
Db 221 -----GKFKGDSVFTSLGTNSG-----SQGGTFSGLL 249

RESULT 32
S70908
transferrin-binding protein 2 precursor - Haemophilus influenzae (strain SB29)
C:Species: Haemophilus influenzae
A:Variety: strain SB29
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S70908; S73321
R;Locmore, S.M.; Yang, Y.; Coleman, D.C.; Shortreed, J.M.; England, D.M.; Harkness, R.E.
Mol. Microbiol. 19, 575-586, 1996
A:Title: Cloning and expression of the Haemophilus influenzae transferrin receptor genes.
A:Reference number: S70901; MUID:96228706; PMID:8830248
A:Accession: S70908
A:Molecule type: DNA

A:Residues: 1-631 <LOO>
A:Cross-references: UNIPROT:Q48041; EMBL:U15055
A:Experimental source: strain SB29, clone DS-1090-3-2
R:Loosmore, S.M.
submitted to the EMBL Data Library, September 1994
A:Reference number: S73320
A:Accession: S73321
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-250, 'L', 252-349, 'RTDATTN', 357-631 <LOW>
A:Cross-references: EMBL:U15055; NID:G1223948; PIDN:AA43931.1; PID:G1223949
A:Experimental source: strain SB29, clone DS-1090-3-2
C:Genetics:
A:Gene: tbp2
A:Superfamily: bacterial pathogen transferrin-binding protein; tonB-dependent receptor
F:1-17/Domain: signal sequence #status predicted <SIG>
F:18-631/Product: transferrin-binding protein 2 #status predicted <MAT>

Query Match 7.6%; Score 94.5; DB 2; Length 631;
Best Local Similarity 20.8%; Pred. No. 7.4;
Matches 52; Conservative 28; Mismatches 55; Indels 115; Gaps 11;

Qy 31 YNKEAITENKESDDQFLENTL-----LPKGP-----FTCHPWYNDL----- 67
Db 202 YNRRSAISDIDN-----LENNLKGAGLTSEFTVNGTKLTKGLYNERETNNNKLQKR 257
Qy 68 ---LVDLGSKDATNKYKGK-----KVDLYGAYGYQCAGGTPNKTAQMY 108
Db 258 KHELVDIDADIYSNFRGKVKPTTKDSQEHFTSEGLEGGFYG-----PNGEE--L 308
Qy 109 GGVTLHDNNRL-----TEKKVPINLWIDGKQTTVPIDK-----VKTSSKEV 150
Db 309 GCKFLAGDNRVGVFSAKEETKDKLSRETLIDGKLIFFTKTKTDAKTAANAKTDEKNF 368
Qy 151 TVQELD-----LQARHYLHG-----KFG 168
Db 369 TTKDIPSGEADYLLIDNVFPLFPBENTNDFITSRHHKVGDKTVKVEACCKNLVYVRF 428
Qy 169 LYNSSPFGK 178
Db 429 MYTEDPLNGE 438

RESULT 33
C99803
Hypothetical protein SA0357 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: C89803
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: C89803
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-203 <KUR>
A:Cross-references: UNIPROT:Q99WK7; GB:BA000018; PID:G13700284; PIDN:BAB41582.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA0357

Query Match 7.6%; Score 94; DB 2; Length 203;
Best Local Similarity 21.5%; Pred. No. 1.9;
Matches 51; Conservative 34; Mismatches 52; Indels 100; Gaps 12;

Qy 1 SEKSEBINEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTG 60
Db 37 TQNSSVQDKLQKQVEVPNN-----SEKALVKK----- 65
Qy 61 HPWYNLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTA-CMYGGVTLHDNNRL 119

Db 66 -----LYDRYSKDTIN-----GKSNKSRNWYSEPLNEQ-- 96
Qy 120 TEKKVPINLWIDGKQTTVPIDKVKTSKE-----VTQELDLQARHYLHGKFLYNS 172
Db 97 -----VRIHLEGTYYTA--DRVYTPKRNITLKEVVTLKELDHIR-FAHSYGLY-- 144
Qy 173 DSFGKVGQGLIVFHSSEGSTVSVDLFDAAQGYPTL-----LRIYRONKNTINSENL 224
Db 145 --MGSHLPKGNIVINTKDG-----GKY--TLESHKELQKRENVKINTADI 186

RESULT 34
G89806
exotoxin 6 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G89806
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: G89806
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-226 <KUR>
A:Cross-references: UNIPROT:Q99WT1; GB:BA000018; PID:G13700312; PIDN:BAB41610.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:
A:Gene: set6
C:Superfamily: toxic shock syndrome toxin

Query Match 7.6%; Score 94; DB 2; Length 226;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 49; Conservative 38; Mismatches 63; Indels 68; Gaps 11;

Qy 8 NEKDLRKKSELQNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFFTGHPW-- 63
Db 24 NVQSVQAKTEVKQOSESELK--HYTN-KPVLERN-----VTGYKYTEKG 65
Qy 64 --YNDLLVD-----LGS-KDAATNKYKGVLDLYGAYGYQCAGGTPNKTAQMYGGVT 112
Db 66 KDYIDVIDVNOYQSISLVGSKDKPKGDSNIDVF-----ILREGDSRQATNYSIGGVT 120
Qy 113 LHDNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKE-----VTQELDLQAR 160
Db 121 -----KTNSQPFIDYIHT--PILEIKKKEEPOSSLYQIYKEDISUKELDYRLR 167
Qy 161 HVLHGKFLYNSDSFGKVGQGLIVFHSSEGSTVSVDL 198
Db 168 ERAIKQHGLYSNG-----LKQSQIITMKDGKSHITDL 200

RESULT 35
DVZQF
Multidrug resistance protein - malaria parasite (Plasmodium falciparum)
N:Alternate names: P-glycoprotein
C:Species: Plasmodium falciparum
C:Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C:Accession: S18204; A32547
R:Triglia, T.; Foote, S.J.; Kemp, D.J.; Cowman, A.F.
Mol. Cell. Biol. 11, 5244-5250, 1991
A:Title: Amplification of the multidrug resistance gene pfmdr1 in Plasmodium falciparum
A:Reference number: S18204; MUID:92017800; PMID:1922044
A:Accession: S18204
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-1419 <TRI>
A:Cross-references: UNIPROT:PI3568; EMBL:X56851; NID:G9935; PIDN:CAA0180.1; PID:G9936
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1990
R:Foote, S.J.; Thompson, J.K.; Cowman, A.F.; Kemp, D.J.

A:Accession: A1161
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <GLA>
A:Cross-references: UNIPROT:Q92DV7; GB:NC_003210; PIDN:CAC98775.1; PID:G16410086; GSPDB:
A:Experimental source: strain EGD-e
C:Genetics:
A:Gene: lmo0697

Query Match 7.3%; Score 90; DB 2; Length 411;
Best Local Similarity 20.9%; Pred. No. 10;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;
QY 32 YNEKAITENKESDDQFLENTL--LFGGFFTG-HPW-----YNDLLVD--LGSKDATNK 79
DB 34 YKQSVFVN-----DLLYQNTMGSVAGGLYAGTNPMSFGSGKIGAILTDYTAGSPSTGR 89
QY 80 YGKKVDLYGAYGYQCAGGTNPNTACMGVGTLLHNNRLTEK----- 123
DB 90 NKDAALQGRGFFIAGDNAGG--NIVVTRDGSFAVSDNNYLTTOQGYVMGYATDKNGNVL 147
QY 124 -----KVPINLWDGKOT-----TVPIDKVTSSKEVTVOELDLQARHYLHGKFG 169
DB 148 NGNLOPIQIPLNSAIPGEATKNGSLSGNIPLD---WGEKDTISSELSVY----- 193
QY 170 YNSDSFGG--KVQRGLIVFHSSEGSTVSVDL-----FDAQGY--PD 207
DB 194 ---DNAGGKHKLQVNMKAATPDASGNVSVEYEIQMDGKALTPPVGTGLNLYNAQGLTNP 250
QY 208 TLLRIYRDNKTINSENHLIDLVL 230
DB 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 39
A11520
Flagellar hook protein FlgE homolog lin0705 [imported] - Listeria innocua (strain Clip11
C:Species: Listeria innocua
C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004
C:Accession: A11520
R:Glaser, P.; Frangoul, L.; Buchrieser, C.; Anand, A.; Baquero, F.; Berche, P.; Bloeker
; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Duesurget, O.; Entian, K.D.; Fsihi, H.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A:Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kuxapkat, G.; Madueno, E.; Maitournam, A.; Ma
ok, C.; Schluter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,
A:Title: Comparative genomics of Listeria species.
A:Reference number: AB1077; MUID:21537279; PMID:11679669
A:Accession: A11520
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-411 <GLA>
A:Cross-references: UNIPROT:Q92DV7; GB:AL592022; PIDN:CAC95937.1; PID:G16413157; GSPDB:
A:Experimental source: strain Clip11262
C:Genetics:
A:Gene: lin0705

Query Match 7.3%; Score 90; DB 2; Length 411;
Best Local Similarity 20.9%; Pred. No. 10;
Matches 55; Conservative 39; Mismatches 81; Indels 88; Gaps 14;
QY 32 YNEKAITENKESDDQFLENTL--LFGGFFTG-HPW-----YNDLLVD--LGSKDATNK 79
DB 34 YKQSVFVN-----DLLYQNTMGSVAGGLYAGTNPMSFGSGKIGAILTDYTAGSPSTGR 89
QY 80 YGKKVDLYGAYGYQCAGGTNPNTACMGVGTLLHNNRLTEK----- 123
DB 90 NKDAALQGRGFFIAGDNAGG--NIVVTRDGSFAVSDNNYLTTOQGYVMGYATDKNGNVL 147
QY 124 -----KVPINLWDGKOT-----TVPIDKVTSSKEVTVOELDLQARHYLHGKFG 169
DB 148 NGNLOPIQIPLNSAIPGEATKNGSLSGNIPLD---WGEKDTISSELSVY----- 193

QY 170 YNSDSFGG--KVQRGLIVFHSSEGSTVSVDL-----FDAQGY--PD 207
DB 194 ---DNAGGKHKLQVNMKAATPDASGNVSVEYEIQMDGKALTPPVGTGLNLYNAQGLTNP 250
QY 208 TLLRIYRDNKTINSENHLIDLVL 230
DB 251 ALKNI-QINSTVNGKQVNMGLNL 272

RESULT 40

F82884
hypothetical protein UU495 [imported] - Ureaplasma urealyticum
C:Species: Ureaplasma urealyticum
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82884
R:Glass, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H.
submitted to GenBank, February 2000
A:Description: The complete sequence of Ureaplasma urealyticum: Alternate views of a mini
A:Reference number: A82870
A:Accession: F82884
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-5005 <GLA>
A:Cross-references: GB:AE002148; GB:AF222894; NID:G68999495; PIDN:AAF30907.1; GSPDB:GN001;
A:Experimental source: serovar 3; biovar 1
C:Genetics:
A:Gene: UU495
A:Genetic code: SGC3

Query Match 7.3%; Score 90; DB 2; Length 5005;
Best Local Similarity 21.2%; Pred. No. 2.3e+02;
Matches 62; Conservative 40; Mismatches 113; Indels 78; Gaps 12;
QY 7 INEKLRKKSELQRNALNLR-----QIYYNEKAITENKESDDQFLENTLFLKGF 58
DB 1494 VNKLDTNLSLQNFSPSNKPNHLYRLKVVYGDQNFDAINEQKNILALNPSLVNSF 1553
QY 59 TGHP-----WYNDLLVDLGSKDATNK-YGKKVDLYGAYGYQCAGGP----- 101
DB 1554 STTPAKIKVSKNAIDVQWQNALIKLILDDSDNLHSGDEININRIKGTQNIISTPATIS 1613
QY 102 -----NKTACM-----YGVTLHDNNLT-----BEKKVPINLWDG---KQTT 137
DB 1614 DQDKRYTKMATNLGIADLYEIVSVTIKQKTNVSPFIPELPSGPIGYTLAPVKFITS 1673
QY 138 VPIDKVTSSKEVTVOELDLQARHYLHGKFGLYNSD-----SFGGKYQVQGL 183
DB 1674 LMDPVYHENKNTADLKINLRINI---GASLFNKDKIKFIFKRNKDGKQISFIHKVT--- 1727
QY 184 IVFHSSEGSTVSVDLFDAGQYVDTLLR-IYRDNKTINSENL-----HIDLVL 231
DB 1728 ----SANDANYEWEFFKLLRNREYTLERVVYLKKNKDFNQSNVSESDYIDLWIY 1776

RESULT 41

G71615
phospholipase A2-like a/b fold hydrolase PFB0410c - malaria parasite (Plasmodium falcipar
C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 09-Jul-2004
C:Accession: G71615
R:Gardner, M.J.; Tettelin, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;
; Pertea, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.;
Science 282, 1126-1132, 1998
A:Title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9804551
A:Accession: G71615
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-679 <GAR>
A:Cross-references: UNIPROT:O96176; GB:AE001393; GB:AE001362; NID:G3845175; PIDN:AAC71871
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0410c

Db 374 LPEDGVQ-----VQMSRTGKSVTMRDLIEVGLDATRYF---FAMKSSDTHNFDM 423

Qy 176 -----GGKVQRLIVFHSSEGT-----SYDLFDAQGY 205

Db 424 LAKSTSDNPVYVQYAHARISSILRSK-EQGLEVSKDANNSLLETEAEYDLKVLGEF 482

Qy 206 PTLI-----RIYRDNKTINSENLI 226

Db 483 ADVAAEAVKRAPIRVIRYVYNDLATAFHFYNSKNVLDMDNLEV 526

RESULT 57

D86342

C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 16-Aug-2004

C:Accession: D86342

R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Pederspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: D86342

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-614 <STO>

A:Cross-references: GB:AE005172; NID:g4836893; PIDN:AAD30596.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: Pyrophosphate-dependent phosphofructokinase, PfPb type; 6-phosphofructoki

Query Match 6.9%; Score 85; DB 2; Length 614;

Best Local Similarity 30.6%; Pred. No. 42;

Matches 26; Conservative 8; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGGVDLYGAYYQACGTPNKTKMYGGVT-----LHDNNRLTEE 122

Db 412 KEGT--YKGGKFNALCHFFGYQARGSLPSKFCDCYAVVLGHICYHVAAGLNGYMATVN 469

Qy 123 KKPINLWIDGKQTTVPIDKVKTSK 147

Db 470 LKSPVKNW---KCGATPITAMMTVK 491

RESULT 58

T10102

C:phosphate-fructose-6-phosphate 1-phosphotransferase (EC 2.7.1.90) alpha chain - castor

N:Alternate names: 6-phosphofructokinase (pyrophosphate)

C:Species: Ricinus communis (castor bean)

C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004

C:Accession: T10102

R:Todd, J.F.; Blakeley, S.D.; Dennis, D.T.

Gene 152, 181-186, 1995

A:Title: Structure of the genes encoding the alpha- and beta-subunits of castor pyrophos

A:Reference number: Z16949; MUID:95137384; PMID:7835697

A:Accession: T10102

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-617 <FOD>

A:Cross-references: UNIPROT:Q41140; EMBL:Z32849; NID:g483546; PIDN:CAA83682.1; PID:g4835

C:Genetics:

A:Introns: 30/3; 88/2; 126/1; 151/1; 189/1; 211/3; 239/3; 257/3; 284/3; 316/1; 340/3; 37

C:Superfamily: pyrophosphate-dependent phosphofructokinase, PfPb type; 6-phosphofructoki

C:Keywords: phosphotransferase

Query Match 6.9%; Score 85; DB 2; Length 617;

Best Local Similarity 30.2%; Pred. No. 42;

Matches 26; Conservative 9; Mismatches 35; Indels 16; Gaps 3;

Qy 74 KDATNKYKGGVDLYGAYYQACGTPNKTKMYGGVT-----LHDNNRLTEE 122

Db 412 KEGT--YKGGKFNALCHFFGYQARGSLPSKFCDCYAVVLGHICYHVAAGLNGYMATVN 469

Qy 123 KKPINLWIDGKQTTVPIDKVKTSK 148

Db 470 LKNPVNKRWC---AAPIAAMMTVKR 492

RESULT 59

B44858

C:lactococin (EC 3.4.21.96) precursor [validated] - Lactobacillus paracasei (strain NCDO 1;

N:Alternate names: cell-envelope-associated proteinase prtp; serine proteinase Lp151

C:Species: Lactobacillus paracasei

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C:Accession: B44858; C44858; A44850

R:Holck, A.; Naes, H.

J. Gen. Microbiol. 138, 1353-1364, 1992

A:Title: Cloning, sequencing and expression of the gene encoding the cell-envelope-associ

A:Reference number: A44858; MUID:92381481; PMID:1512565

A:Accession: B44858

A:Molecule type: DNA

A:Residues: 1-1902 <HOLL>

A:Cross-references: UNIPROT:Q02470; GB:M83946; NID:g149580; PIDN:AA25248.1; PID:g149582

A:Note: sequence extracted from NCBI backbone (NCBIN:112261, NCBIP:112263)

A:Note: the source is designated as Lactobacillus paracasei subsp. paracasei

A:Accession: C44858

A:Molecule type: protein

A:Residues: 'X', 189-196 <HOL2>

R:Naes, H.; Nissen-Meyer, J.

J. Gen. Microbiol. 138, 313-318, 1992

A:Title: Purification and N-terminal amino acid sequence determination of the cell-wall-1

A:Reference number: A44850; MUID:92226694; PMID:1564442

A:Accession: A44850

A:Status: preliminary

A:Molecule type: protein

A:Residues: 189-196 <NAE>

A:Cross-references: PIDN:AA22052.1; PID:g248666

A:Experimental source: strain NCDO 151

A:Note: sequence extracted from NCBI backbone (NCBIP:94706)

C:Genetics:

A:Gene: prtp

C:Superfamily: lactococin; subtilisin homology

C:Keywords: hydrolase; serine proteinase; transmembrane protein

F:1-23/Domain: signal sequence #status predicted <SIG>

F:23-187/Domain: propeptide #status predicted <PRO>

F:188-1902/Product: serine proteinase, cell-envelope-associated #status experimental <MA>

F:208-634/Domain: subtilisin homology #status atypical <SBT>

Query Match 6.9%; Score 85; DB 1; Length 1902;

Best Local Similarity 25.8%; Pred. No. 1.7e+02;

Matches 51; Conservative 12; Mismatches 69; Indels 66; Gaps 8;

Qy 46 QFLENTLLFK-----GFFTGHPWYNDLLVLDLGSKDATNKYKGGKVDLYGAYG 93

Db 805 QFVEGFNFKSGDSRLNLPYMGFGD---WND-----GKIVDSLNG-IT 845

Qy 94 YOCAGTPTNKTKMYGGVTLDHNNRLTEKKVPINLWIDGKQTTVPIDKVKTSKEVTQ 153

Db 846 YSPAGN-----YGTVPLLTNKNTGHQYGGWTDADGKQT----- 881

Qy 154 ELDLQARHYLHGKFGLYNSDSFGGKVGQGLIVFHSSEGSTVSVDLPDAQSQYPTLLRIY 213

Db 882 -VDDQIAFSSDKNALYNDISHWYLLRNI-----SNVQVDILDGQGNKVTLLSS-- 930

Qy 214 RDNKTINSENHLIDLYL 231

Db 931 STNQTKTYDDAHSQKIY 948

Query Match 6.8%; Score 84; DB 2; Length 227;
Best Local Similarity 21.2%; Pred. No. 15;
Matches 48; Conservative 42; Mismatches 90; Indels 46; Gaps 10;
QY 6 EINEKDLRKKSELQNRN---ALSNLRQIYYNEKAITENKESDDQPLENTLLFKGFTGHP 62
DB 34 EVRSQATQDLSEYKGRGFELTNVGYKGNKVTFDNSQQIDVTL-----TG-- 81
QY 63 WYNDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLDHNNRLTEE 122
DB 82 --NEKLTWKDDDEVN-----VDVFVREGSDKSAITTS-----IGGIT-KTNGTQHKD 127
QY 123 KKVPIINLWID---GKOTT-VPIDKVKTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGK 178
DB 128 TVQNVNLSVSKSTGQHTTSVTSEYYSIYKEEISLKELDFKLKHLIDKHDLKYKTEPKDSK 187
QY 179 VQRLGLIVFHSSEGSTVSVDLPDAQOYPTDLRIYRDNKTINSENL 224
DB 188 IR-----ITMKNGGYVTFEL-----NKKLQPHRMGDTIDSRNI 220
RESULT 64
D86671
transposase of IS1077C [imported] - Lactococcus lactis subsp. lactis (strain IL1403)
C:Species: Lactococcus lactis subsp. lactis
C:Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004
C:Accession: D86671
R:Botolin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarne, K.; Weissenbach, J.; Ehrlich
Genome Res. 11, 731-753, 2001
A:Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis se
A:Reference number: A86625; MUID:21235186; PMID:11337471
A:Accession: D86671
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <STO>
A:Cross-references: UNIPROT:09CII18; GB:AE005176; PID:g12723243; PIDN:AAK04470.1; GSPDB:G
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tra1077C

Query Match 6.8%; Score 84; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 18;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;
QY 5 BEINEKDLRKKSELQNRNLSNRQIYYNEKAITENKESDDQPLENTLLFKGFTGHPWY 64
DB 19 ERVNDKELIEKEMLK-----IRQ-----EHANAGYRPMRELLKQRGYHVNHKV 62
QY 65 NDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLDHNNRLTEEKK 124
DB 63 QRLMKKGLRVTSYWHKSRK-----YNSYKGVGTVAKN-----KLHRRFR----- 103
QY 125 VPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLI 184
DB 104 -----TSIPHQKITDTTPEFYEDGIQKCYLNPYALFNSE-----VI 143
QY 185 VFH-SSEGSTVSVDL 198
DB 144 SYHISKQPSQSIDI 158

RESULT 65
F70339
glycerol kinase - Aquifex aeolicus
C:Species: Aquifex aeolicus
C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 09-Jul-2004
C:Accession: F70339
R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; O
V.
Nature 392, 353-358, 1998
A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A:Reference number: A70300; MUID:98196666; PMID:9537320
A:Accession: F70339

A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-492 <AOF>
A:Cross-references: UNIPROT:O66746; GB:AE000690; NID:g2983100; PIDN:AAO6710.1; PID:g298;
A:Experimental source: strain VF5
C:Genetics:
A:Gene: gipk
C:Superfamily: xylokinease
Query Match 6.8%; Score 84; DB 2; Length 492;
Best Local Similarity 25.7%; Pred. No. 39;
Matches 61; Conservative 30; Mismatches 74; Indels 72; Gaps 15;
QY 9 EKDLRKKSELQNRNLSNRQ---IYYNEKAITENKESDDQPLENTLLFKGFTGHPWYN 65
DB 44 EQDPLELWEAVRKSLSSEVIQQVGLKEINSIGITNORE-----TVILWDKETGRPVYN 95
QY 66 DLL-VDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMYGGVTLDHNNRLTEEKK 124
DB 96 AILWDLRTEDIC-----RKLSEYSEYIKENT-----GLLLHPYFSASK--- 134
QY 125 VPINLWIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGK---FGLYNS-----DSFGK 178
DB 135 --VN-WI-----IENVGVKKDIE-----RGKVIETGVTWILWNLTGSK 171
QY 179 VQRLGLIVFHSSEGSTVSVD-LFDAQG-QYPTDLRIYRDNKTINSE-NLHIDLXYLT 232
DB 172 V-----HKTEPSNASRTLLFNIRKLEYDDELLKIFRIPKNILPEVNNESSLFGVT 221
RESULT 66
T41863
chitinase chi-A orf126 - Bombyx mori nuclear polyhedrosis virus (isolate T3)
C:Species: Bombyx mori nuclear polyhedrosis virus, BmsNEV
A:Variety: isolate T3
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C:Accession: T41863
R:Gomi, S.; Majima, K.; Maeda, S.
J. Gen. Virol. 80, 1323-1337, 1999
A:Title: Sequence analysis of the genome of Bombyx mori nucleopolyhedrovirus.
A:Reference number: Z22020; MUID:99281911; PMID:10355780
A:Accession: T41863
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-552 <KAM>
A:Cross-references: UNIPROT:O92482; EMBL:L33180; NID:g3745835; PIDN:AAC63792.1; PID:g374;
A:Experimental source: isolate T3
C:Superfamily: Serratia marcescens chitinase
Query Match 6.8%; Score 84; DB 2; Length 552;
Best Local Similarity 24.3%; Pred. No. 45;
Matches 45; Conservative 23; Mismatches 69; Indels 48; Gaps 11;
QY 32 YNEKAI---TENKESDDQPLENTLLFKGFTGHPWYNLLVDLGSKDATNKYKGGKVDLY 88
DB 359 YDKIAVAVYAEAKSLDKIFLMTYDFK-----AWSN---TDLGYQTTVYAPSWNSEELY 410
QY 89 GAYGYQC---AGGTPNKT---ACMYG---GVTLHDN-NRLTEEKKVPIN-LWIDGKQT 136
DB 411 TTHYAVDALLEGQVDPNKLIVGVAMRGWGTGVTYTNNGYFSGTNGPVGSGTWEDG--- 467
QY 137 TVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQRLIVFHSSEGSTVS 196
DB 468 -----VDYRQIQKDLNNY-----VYTFDS-----AAQASYVFDKSKGLDISF 505
QY 197 DLFDA 201
DB 506 DSVDS 510

RESULT 67

T44118

penicillin-binding protein 2 [imported] - Staphylococcus aureus

C:Species: Staphylococcus aureus
C:Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 09-Jul-2004
C:Accession: T44118
R:Ito, T.; Katayama, Y.; Hiramatsu, K.
Antimicrob. Agents Chemother. 43, 1449-1458, 1999
A:Title: Cloning and nucleotide sequence determination of the entire mec DNA of pre-meth-resistant Staphylococcus aureus
A:Reference number: 222733; MUID:99278010; PMID:10348769
C:Accession: T44118
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-668 <IT>
A:Cross-references: UNIPROT:Q54113; EMBL:D86934; PIDN:BAAB2220.1
A:Experimental source: strain N315
C:Genetics:
A:Note: mecA
C:Superfamily: penicillin-binding protein 2B

Query Match 6.8%; Score 84; DB 2; Length 668;
Best Local Similarity 20.0%; Pred. No. 57;
Matches 63; Conservative 45; Mismatches 87; Indels 120; Gaps 15;

Qy 4 SEEINEKDLRKKE---LQNALSNLRQIYYNEK-----AITE 39
Db 261 SEELKQKEYKGKDDAVIGKKGLEK-----YDKLQHEHGGRVTIVDDNSNTIAHTLIE 315
Qy 40 NKESDDQPLENTLLFKGFTGHPWYNLLVLDLGSKDATNKYKKVDL-----YGAYYGY 94
Db 316 KKKKDGKDIQTIDAK---VQKSYNNKNDYSGSTAIHPOTGELLALVSTPVDVY--- 369
Qy 95 QCAGGTPNKTACMGVGTLDHNNRLTEKKVP-INLWIDGKQTTP--IDKVTSSKEVT 151
Db 370 -----PFMY-GMSNEEYNKLTEDKPELNKP---QITTSPTSQTILTAMIGLN 415
Qy 152 VQELDLQARHYLHCKFGLYNSDSFG----- 177
Db 416 NKTLDKTSYKIDGK-GWQKDKSWGYNVTRYEVVNGNIDLKQAISSDNIFARVALEL 474
Qy 178 ---KVQGLIVFHSSEGSTSYDLFDAQ-----GO-----YPTDLLRI 212
Db 475 GSKFEKGMKGLGVGEDIPSDYPFNAQISKNKLDNEILLADSGVGQGEILINPVQILSI 534
Qy 213 Y---RDNKTINSENL 224
Db 535 YSALENNGNINAPHL 549

RESULT 68
JQ0773
penicillin-binding protein mecA, low-affinity - Staphylococcus aureus
N:Alternate names: MRSA PBP; penicillin-binding protein 2'
C:Species: Staphylococcus aureus
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0773; S00092
R:Ryffel, C.; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser, F.
Gene 94, 137-138, 1990
A:Title: Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus
A:Reference number: JQ0773; MUID:91033056; PMID:2227446
C:Accession: JQ0773
A:Molecule type: DNA
A:Residues: 1-668 <RYF>
A:Cross-references: UNIPROT:Q53707; GB:X52593; NID:g46610; PIDN:CAA36829.1; PID:g46611
R:Song, M.D.; Wachi, M.; Doi, M.; Ishino, F.; Matsuhashi, M.
FEBS Lett. 221, 167-171, 1987
A:Title: Evolution of an inducible penicillin-target protein in methicillin-resistant Staphylococcus aureus
A:Reference number: S00092; MUID:87304805; PMID:3305073
C:Accession: S00092
A:Molecule type: DNA
A:Residues: 1-245, 'G', 247-302, 'RV', 303-609, 'T', 611-668 <SON>
A:Cross-references: EMBL:Y00688; NID:g46628; PIDN:CAA68684.1; PID:g46629
R:Hiramatsu, K.; Asada, K.; Suzuki, E.; Okonogi, K.; Yokota, T.
FEBS Lett. 298, 133-136, 1992
A:Title: Molecular cloning and nucleotide sequence determination of the regulator region of the mec operon of methicillin-resistant Staphylococcus aureus
A:Reference number: S20574; MUID:92183847; PMID:1544435

A:Accession: S20574
A:Status: translation not shown
A:Molecule type: DNA
A:Residues: 1-41 <HIR>
A:Cross-references: EMBL:X63598; NID:g46612; PIDN:CAA5141.1; PID:g46613
C:Comment: Enzymes involved in cell wall synthesis are the primary target of beta-lactam resistant Staphylococcus aureus" (MRSA) has a very low affinity to beta-lactam antibiotic C:Genetics:
A:Gene: mecA
A:Note: the gene for this protein contains a penicillin-inducible promoter, resulting in a cell wall synthesis gene may have evolved by gene fusion; the amino end (pos 1-60) is a penicillin binding protein part is neither from S. aureus nor from E. coli
C:Superfamily: penicillin-binding protein 2B
C:Keywords: antibiotic resistance; cell wall synthesis
F:403/Active site: Ser #status predicted

Query Match 6.8%; Score 84; DB 2; Length 668;
Best Local Similarity 20.0%; Pred. No. 57;
Matches 63; Conservative 45; Mismatches 87; Indels 120; Gaps 15;

Qy 4 SEEINEKDLRKKE---LQNALSNLRQIYYNEK-----AITE 39
Db 261 SEELKQKEYKGKDDAVIGKKGLEK-----YDKLQHEHGGRVTIVDDNSNTIAHTLIE 315
Qy 40 NKESDDQPLENTLLFKGFTGHPWYNLLVLDLGSKDATNKYKKVDL-----YGAYYGY 94
Db 316 KKKKDGKDIQTIDAK---VQKSYNNKNDYSGSTAIHPOTGELLALVSTPVDVY--- 369
Qy 95 QCAGGTPNKTACMGVGTLDHNNRLTEKKVP-INLWIDGKQTTP--IDKVTSSKEVT 151
Db 370 -----PFMY-GMSNEEYNKLTEDKPELNKP---QITTSPTSQTILTAMIGLN 415
Qy 152 VQELDLQARHYLHCKFGLYNSDSFG----- 177
Db 416 NKTLDKTSYKIDGK-GWQKDKSWGYNVTRYEVVNGNIDLKQAISSDNIFARVALEL 474
Qy 178 ---KVQGLIVFHSSEGSTSYDLFDAQ-----GO-----YPTDLLRI 212
Db 475 GSKFEKGMKGLGVGEDIPSDYPFNAQISKNKLDNEILLADSGVGQGEILINPVQILSI 534
Qy 213 Y---RDNKTINSENL 224
Db 535 YSALENNGNINAPHL 549

RESULT 69
JQ0774
penicillin-binding protein mecA, low-affinity - Staphylococcus epidermidis
N:Alternate names: penicillin-binding protein 2'
C:Species: Staphylococcus epidermidis
C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 09-Jul-2004
C:Accession: JQ0774
R:Ryffel, C.; Tesch, W.; Birch-Machin, I.; Reynolds, P.E.; Barberis-Maino, L.; Kayser, F.
Gene 94, 137-138, 1990
A:Title: Sequence comparison of mecA genes isolated from methicillin-resistant Staphylococcus aureus
A:Reference number: JQ0773; MUID:91033056; PMID:2227446
C:Accession: JQ0774
A:Molecule type: DNA
A:Residues: 1-668 <RYF>
A:Cross-references: UNIPROT:Q54113; GB:X52592; NID:g46993; PIDN:CAA36828.1; PID:g46994
A:Experimental source: strain WT55
C:Genetics:
A:Gene: mecA
C:Superfamily: penicillin-binding protein 2B
F:403/Active site: Ser #status predicted

Query Match 6.8%; Score 84; DB 2; Length 668;
Best Local Similarity 20.0%; Pred. No. 57;
Matches 63; Conservative 45; Mismatches 87; Indels 120; Gaps 15;

Qy 4 SEEINEKDLRKKE---LQNALSNLRQIYYNEK-----AITE 39

```
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-319 <PAR>
A:Cross-references: UNIPROT:Q9PI52; GS:AL139075; GB:AL111168; NID:g6967817; PIDN:CAB75094
A:Experimental source: serotype O2, strain NCTC 11168
C:Genetics:
A:Gene: Cj0456c
C:Superfamily: Campylobacter jejuni hypothetical protein Cj0456c
```

Query Match 6.7%; Score 83.5; DB 2; Length 319;
Best Local Similarity 20.5%; Pred. No. 25;
Matches 58; Conservative 44; Mismatches 112; Indels 69; Gaps 12;

QY 2 EKSEINE--KDLRKSELORNAL-----SNLRQIYYNEKAITENKESDDOF 47
 :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::
DB 44 DKSLENLEYIKNLSPHFLFYHTALFLDAKEOGLPSTNIODCEHENIGKIS----LQHIL 99

QY 48 LENTLLPKGFTGH-PWVNDLLVDLGSKDAT-----NKYKGKKVD---LYGAYYG 93
 :|:::~::~||:::||:::~::::~::::~::::~::::~::::~::
DB 100 LNNAVTTA--TEHYEVSLEFSGRLDFLYSFPALLYNMOKEQPDQLLLVGFKQG 157

QY 94 YQCAGGTGNKTACMGYGVTLHDNN-----RLTEEKVVPINLWDGKQTTP-IDVKVTSSK 147
 ||:::~::::~::::~::::~::::~::::~::::~::::~::
DB 158 YLLAIIVAKNTIIYGDFFKIPEQEELGLELPSEDNQEIENNDDTETVLDNFNALNNK 217

QY 148 KEVTVOBELDQ-----ARHYLHGKFGLYNSFSFGKVVQRGLIV 185
 ::||:::|:::~::::~::::~::::~::::~::::~::::~::
DB 218 FDLDQQENLETLLDNDNFNLDELNQSFSDMELCRYLIITSIEKFYNDDKYAGVFINGILL 277

QY 186 FHSEGTSVSDLFDQAQQYPDTLLRIVRDKNTINSENHLIDL 228
 |:::~::::~::::~::::~::::~::::~::::~::::~::
DB 278 YSESMDINAIDFLES-----ETFLEI-KTKQNLTOLMIHEL 313

RESULT 72
T03276
GAG protease - yeast (Candida albicans) retrotransposon pCal
C:Species: Candida albicans
C>Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C:Accession: T03276
R:Matthews, G.D.; Goodwin, T.J.D.; Butler, M.I.; Berryman, T.A.; Poulter, R.T.M.
J. Bacteriol. 179, 7118-7128, 1997
A>Title: pCal, a highly unusual Ty1/copia retrotransposon from the pathogenic yeast Cand
A:Reference number: Z14877; PMID:98037512; PMID:9371461
A:Accession: T03276
A:Status: preliminary; translated from GB/EMBL/DBIJ
A:Molecule type: DNA
A:Residues: 1-324 <MAT>
A:Cross-references: UNIPROT:O13307; EMBL:AF007776; NID:g2636718; PIDN:AAC49879.1; PID:g26
C:Genetics:
A-Mobile element: retrotransposon pCal

Query Match 6.7%; Score 83.5; DB 2; Length 324;
Best Local Similarity 25.8%; Pred. No. 25;
Matches 42; Conservative 29; Mismatches 61; Indels 31; Gaps 10;

QY 1 SEKSEEINKDLRKSELORNAISLNLRQ-----IYYNE--KAITENKESDDQFLE 49
 |:::~::::~::::~::::~::::~::::~::::~::::~::
DB 3 SAKNDD-NEGKMVESVD-QANAISKVDEHIKARFNMLFIKPNLDPLKLVGNQSVCKWNE 60

QY 50 NTLLFKGFPGFTGHWPVNVDLLVDLGSKDATNYKGGKDYLGYAVGYQCAGGTNPNTACMYG 109
 ||:::~::::~::::~::::~::::~::::~::::~::::~::
DB 61 E---FKYFHVAYPDVEFLDYNPKN---KFKVKKVE-GIYFTGWCL-----QMCLQ- 105

QY 110 GVTLHDNRRTEEKKVPINLWDGKQTTPVIDKVTSSKKEVTV 152
 :|:::~::::~::::~::::~::::~::::~::::~::::~::
DB 106---SIHDRPRLLIMSKLPKHLOKEANLIKAAVDAT-TKSKDYTI 145

RESULT 73
S36595
Li protein - human papillomavirus type 9
C:Species: human papillomavirus type 9

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C;Accession: G36595
R;Delius, H.; Hofmann, B.
submitted to the EMBL Data Library, August 1993
A;Description: Primer-directed sequencing of human papillomavirus types.
A;Reference number: S36469
A;Accession: G36595
A;Molecule type: DNA
A;Residues: 1-507
A;Cross-references: UNIPROT:Q02480; EMBL:X74464; NID:g397068; PIDN:CAA52488.1; PID:g3970
C;Superfamily: papillomavirus L1 protein
C;Keywords: late protein

Query Match 6.7%; Score 83.5; DB 2; Length 507;
Best Local Similarity 20.3%; Pred. No. 44;
Matches 49; Conservative 38; Mismatches 69; Indels 85; Gaps 14;

Qy 42 ESDQFLENTLFP-----KGFTGHPWYNLLVDLGSKD-----ATNKYKGGKVD 86

Db 23 QSTDEYVERTNIFYHAISDRLLTVGHPYV-----DVRSGDQRIEVPKVGNGQVRAFRIS 77

Qy 87 -----LYGAYGYQCAGGTP-----NKTACMYG 109

Db 78 LPDNRFPALAMSVNPKELVWACRIETGRQPLGVGTSGHPLFNKVRDTSNSNYQ 137

Qy 110 GVTLHDNNRLTEBKVPINLWIDGKQTTVP-----DKVTKSKKEVTVQELD-----QAR 160

Db 138 GTTWDRQNTSFDPK-QVQMFIIIG---CIPCLGEHWKAKVCEKXAN-NQLGLCPPIELR 192

Qy 161 HYLHGKFGLYNSDFG---GKVQGLIVFHSSEGSTVSYDLFDAGQVDPDILLR---IYR 214

Db 193 NTV-----IEDGDMFDIGFGNINNKLSEFNKSD---VSLDIVDETCKYPDPLTMANDVYG 244

Qy 215 D 215

Db 245 D 245

RESULT 74

AF1418

ABC transporter, ATP-binding protein homolog lmo2751 [imported] - Listeria monocytogenes

C;Species: Listeria monocytogenes

C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 09-Jul-2004

C;Accession: AF1418

R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker

D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussauguet, O.; Entian, K.D.; Fsihi, H.

Science 294, 849-852, 2001

ok, C.; Schluteter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; Voss, H.; Wehland,

A;Title: Comparative genomics of Listeria species.

A;Reference number: AB1077; MUID:21537279; PMID:11679669

A;Accession: AF1418

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-573 <GLA>

A;Cross-references: UNIPROT:Q8Y3T0; GB:NC_003210; PIDN:CAB00964.1; PID:g16412251; GSPDB:

A;Experimental source: strain EGD-e

C;Genetics:

A;Gene: lmo2751

C;Superfamily: Escherichia coli ABC transporter mdla; ATP-binding cassette homology

Query Match 6.7%; Score 83.5; DB 2; Length 573;

Best Local Similarity 23.3%; Pred. No. 51;

Matches 45; Conservative 30; Mismatches 81; Indels 37; Gaps 8;

Qy 22 ALSNLRQI--YYNEKAITENKESDDQFLENTLFPKGF---FTGH--PWYNLLVD----- 70

Db 298 ALISLKRITEVLETPDITYNENAPEQDLGTEVFRNVSFKYDGDTPDALEDISFKASVG 357

Qy 71 --LGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMGYGVTLHDNNRLTEBKVPIN 128

Db 358 EMVGIVGATGSGKSTLAQLIPRLY-----DPTGEVIGGTNLKDKINKKTLRSTVSFV 410

Qy 129 LWIDGKQTTVPIDKVTKSKKEVTVQELD-----LQARHYLHGKFGLYNS-----DSFGG 177

Db 411 LQRAILFSGTIADNLRHGKDKDAEEMEHASKIAQAKEFIDKQAKLYEAPVSRGNNPSG 470

Qy 178 -----KVQRLGI 184

Db 471 GQKQLRSITRGVI 483

RESULT 75

I83350

outer membrane usher protein csaD precursor - Escherichia coli

C;Species: Escherichia coli

C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C;Accession: I83350

R;Willshaw, G.A.; Smith, H.R.; McConnell, M.M.; Rowe, B.

FEMS Microbiol. Lett. 49, 473-478, 1998

A;Title: Cloning of genes encoding coli-surface (CS) antigens in enterotoxigenic Escheric

A;Reference number: I60266

A;Accession: I83350

A;Status: preliminary; translated from GB/EMBL/DBJ

A;Molecule type: DNA

A;Residues: 1-819 <RES>

A;Cross-references: UNIPROT:P53512; EMBL:U04844; NID:g442375; PIDN:AAC45096.1; PID:g44237

C;Superfamily: outer membrane usher protein fimb

C;Keywords: membrane protein

Query Match 6.7%; Score 83.5; DB 1; Length 819;

Best Local Similarity 21.4%; Pred. No. 80;

Matches 54; Conservative 35; Mismatches 102; Indels 61; Gaps 11;

Qy 12 LRKKSSEL-QRNALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWYNLLVD 70

Db 201 LRNRFEFNQNDKKTWERNYILEKSFYDKK-----LNLIVGESYTSNNYNNYSFTG 253

Qy 71 LGSKDATNKYKGVLDLYGAYGYQCAGGTPNKTCACMGYGVTLHDNNRLTEBKVP----- 126

Db 254 ISVSTDMDVTPSEIDVTPEIHG-----VADSDSQIIVRQGNITIIINESVPAGPF 303

Qy 127 ----INLWIDGKQTTVPIDKVTKSKKEVTV-----QELDLQARHYLHGK----- 166

Db 304 SFPITNLMTYGGQLGNVEITDIYGNKKQYTVSNSSLPLVMRKAGLMVYINPISGLTKKNSD 363

Qy 167 -----FGL-YNDSDFGKVGQRLIVFHSSEGSTVSYDLFDAGQVDPDILLIYRD 215

Db 364 GDFFAQGDINYGTHYNSTLFGG-YQFSKNYFNLSGT--IGTDL----GFSCAWLLNVRS 416

Qy 216 N-KTINSENLIH 226

Db 417 NFKDKNGYNINL 428

RESULT 76

C86884

transposase of ISI077F [imported] - Lactococcus lactis subsp. lactis (strain IL1403)

C;Species: Lactococcus lactis subsp. lactis

C;Date: 23-Mar-2001 #sequence_revision 23-Mar-2001 #text_change 09-Jul-2004

C;Accession: C86884; C86893; H86727

R;Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Ehrlic

Genome Res. 11, 731-753, 2001

A;Title: The complete genome sequence of the lactic acid bacterium Lactococcus lactis ssp

A;Reference number: A86625; MUID:21235186; PMID:11337471

A;Accession: C86884

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-272 <STO>

A;Cross-references: UNIPROT:Q9CB06; GB:AB005176; PID:g12725128; PIDN:AAK06173.1; GSPDB:G

A;Experimental source: strain IL1403

A;Accession: C86893

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-272 <ST2>

A:Cross-references: GB:AE005176; PID:g12725206; PIDN:AAK06245.1; GSPDB:GN00146
A:Experimental source: strain IL1403
A:Accession: H86727
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-272 <ST3>
A:Cross-references: GB:AE005176; PID:g12723748; PIDN:AAK04922.1; GSPDB:GN00146
A:Experimental source: strain IL1403
C:Genetics:
A:Gene: tral077F; tral077G; tral077E

Query Match 6.7%; Score 83; DB 2; Length 272;
Best Local Similarity 21.5%; Pred. No. 22;
Matches 42; Conservative 30; Mismatches 67; Indels 56; Gaps 7;
QY 5 EBINEKDLKSELQALSNLRQIYYNEKAITENKESDDQFLENTLLFKGFTGHPWY 64
DB 19 ERVNDKLEKEMLK-----TRQ-----EHANAGYRPMRELLKQRGVYHNVKKV 62
QY 65 NDLLVDLGSKDATNKYKGGKVDLYGAYGYQCAGGTPNKTACMGYGVTLHDNNRLTEKK 124
DB 63 QRLMKKGLRVTSYWHKSRK-----YNSYKGVGTVAQN-----KLHRRFR----- 103
QY 125 VPINLWIDGKQTVPIPDVKTSKKEVTVQELDLQARHYLHGKFLYNSDSFGKQVORGLI 184
DB 104 -----TSIPHQKITTDTEPKYEDGKQKCYLNPYIDLNSE-----VI 143
QY 185 VFH-SSEGSTVSD 198
DB 144 SYHISKQPSYQSIDI 158

RESULT 77
C83996
hypothetical protein BH2771 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: C83996
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: A83650; MUID:20512582; PMID:11058132
A:Accession: C83996
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-379 <STO>
A:Cross-references: UNIPROT:Q9K979; GB:AP001516; GB:BA000004; MID:g10175192; PIDN:BA064
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH2771

Query Match 6.7%; Score 83; DB 2; Length 379;
Best Local Similarity 29.3%; Pred. No. 34;
Matches 27; Conservative 14; Mismatches 35; Indels 16; Gaps 3;
QY 8 NEKDLKSELQALSNLRQIYYNEKAITENKESDDQFLENTLLFK-----GFFTGHPW 63
DB 107 SEKGYKRVARLQKYDAATTAQI---NQKADADFAERTSFFENTWYAKNEVAYFTKPM 163
QY 64 YNDLLVDLGSKDATNKYKGGKVDLYGAYGYQ 95
DB 164 IPDLF-----NVCKGRQLVIVARYAGFE 186

RESULT 78
B89986
hypothetical protein SA1774 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89986
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.

Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of meticillin-resistant Staphylococcus aureus.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: B89986
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-381 <KUR>
A:Cross-references: UNIPROT:Q99SS8; GB:BA000018; PID:g13701758; PIDN:BA043051.1; GSPDB:G1
A:Experimental source: strain N315
C:Genetics:
A:Gene: SA1774

Query Match 6.7%; Score 83; DB 2; Length 381;
Best Local Similarity 22.6%; Pred. No. 34;
Matches 61; Conservative 34; Mismatches 71; Indels 104; Gaps 15;
QY 9 EKDLAKKSELQALSNLRQIYYNEKA-----ITENKESDDQFL--ENTL--LPKGF 59
DB 43 ETKLQAKAEAEVSSLPKSAQSLNSQSRFFMDINKNVNKEKLLPETIDRIFEDLT 102
QY 60 GHPWYNDLLVDLGSKDATNKYKGGK-----VDLYGAYGY---QCAGGTPNKTACMGV 111
DB 103 NHP-----LLADLGIKNAGLRKFLKSETSGVAVWGKIYGEIKGQLDAFSEETA 153
QY 112 TLHDNNRLTEKKVPINL-----WID-----GKQTVTPIDKVK 144
DB 154 ----QNKLTAFVVLPKDLNDFGPAWIERFVRVQIEBAFAVALETAFLKGTGKQDQIGLNR 209
QY 145 TSKEKVTVOELDLQARHYLHGKFLYNSDSFGKQVORGIVF-----HS 188
DB 210 QVQKGVSVTE-----GAYPE-----KBEQGLTFANPRATVNELTQVPKYHS 251
QY 189 S--EGSTVSYS-----DLFDAQGOY 205
DB 252 TNEKGSVAVGNVTVMVNPSPDAFEVQAOY 281

RESULT 79
A71509
probable transcription termination factor - Chlamydia trachomatis (serotype D, strain UW:
C:Species: Chlamydia trachomatis
C:Date: 13-Sep-1998 #sequence_revision 13-Sep-1998 #text_change 09-Jul-2004
C:Accession: A71509
R:Stephens, R.S.; Kallman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitchell,
Science 282, 754-759, 1998
A:Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia tract
A:Reference number: A71570; MUID:9900809; PMID:9784136
A:Accession: A71509
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-464 <ARN>
A:Cross-references: UNIPROT:O84498; GB:AE001322; GB:AE001273; MID:g3328916; PIDN:AAC68091
A:Experimental source: serotype D, strain UW-3/Cx
C:Genetics:
A:Gene: rho
C:Superfamily: transcription termination factor rho
C:Keywords: transcription termination

Query Match 6.7%; Score 83; DB 2; Length 464;
Best Local Similarity 25.7%; Pred. No. 43;
Matches 62; Conservative 23; Mismatches 64; Indels 92; Gaps 14;
QY 1 SEKSEINEKDLKSELQALSNL-----RQIYYNEKAITENK-----ESDDQ 46
DB 37 TEKETSPQVATKTAQLQRMGINELNVLARQYGVNGLTSKQVVFEIVKAKSERPDE 96
QY 47 FL--ENTL--LPKGF--FTGHPWYN-----DLLV-----DLGSKDA-----TNKYK 81
DB 97 FLIGEVLEVPDGFGLRSPTNYLPSAEDIYVSPAQIRRFDLKGDITVIGTIRSPKEK 156
QY 82 GK-----KVDLYGAYGYQCAGGTPNKT--ACMGYGT--LHDNNRLTEKKVPINLWIDG 133
DB 157 EKYFALLKVD-----KINGSTPDKAKERVLFENLTPLHPNERLIME----- 197

Db 311 ETDQLLN-----NRAKSKVKL-----NVDGVEIETLSLSAT 344
Qy 123 KKVPTNLWDGKQTTVPIDK-----VKTSSKEVTQ-----ELDLQARHYLHGKF 167
Db 345 KVA-WRFDEAKYKRIERALKSLEELKEKLAKIEQIEKQNIKILTKRKEWY----- 399
Qy 168 GLYNSDSFGKQVQG--LIVP--HSSEGSTV-----SYDLF---DAQGQVPTDLLRIYR 214
Db 400 -----EKYRWSISRSGYLILGRDASQNESIVKKYLRDKDIFLHADIIGA-PATII-ITQ 452
Qy 215 DNKTINSENHL 225
Db 453 DNKTISEEDIY 463

RESULT 90
AH0340
putative autotransporter protein yapC [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AH0340
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AH0340
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-638 <KUR>
C:Cross-references: UNIPROT:Q9F290; GB:AL590842; PIDN:CAC93031.1; PID:g15980769; GSPDB:G
A:Genetics:
A:Gene: yapC

Query Match 6.7%; Score 82.5; DB 2; Length 638;
Best Local Similarity 20.5%; Pred. No. 71;
Matches 43; Conservative 22; Mismatches 64; Indels 81; Gaps 7;
Qy 68 LVDLG-----SKDATNKYKGVKVDLYGAYGYQCAGTTPNKTACMYGGVT----- 112
Db 299 VVDLGYYQYGLYSQESNG-----STDWYLATSTELPFTTTPNVTAPMLSSAAQGVNLMAA 353
Qy 113 -----LHNNRLTEEEKVPTNLWDGKQTTV 138
Db 354 APRHILNABELSTLRQGBELKADAEQTVGVWARYLTDDSRSDNKNIAFNLTSGME--I 411
Qy 139 PIDKVKTSKEVTQVQELDLQARHYLHGKFLGYNDSFGKQVQGLIVFHSSSEGSTVSY-- 196
Db 412 GADK-----QLGLNRGNMLIGAFTSYSSSDVKST-----HDANGDIRSYGG 452
Qy 197 ----DLFDAQGYPTDLLRIYRDNKNTINSE 222
Db 453 GLYLTLDQSGFYVDYTLKANRNNKNTQ 482

RESULT 91
AB0122
probable ferric siderophore receptor iutA [imported] - Yersinia pestis (strain CO92)
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AB0122
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A:Reference number: AB0001; MUID:21470413; PMID:11586360
A:Accession: AB0122
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-726 <KUR>

A:Cross-references: UNIPROT:Q8ZHB0; GB:AL590842; PIDN:CAC89837.1; PID:g15979062; GSPDB:G
C:Genetics:
A:Gene: iutA

Query Match 6.7%; Score 82.5; DB 2; Length 726;
Best Local Similarity 25.1%; Pred. No. 83;
Matches 60; Conservative 20; Mismatches 72; Indels 87; Gaps 14;
Qy 51 TLLPKGFTGHPWYNDDLVDLGSKDATNKYKGVKVDLYGAYGYQCAGT-----P 101
Db 130 TSLYGGSGTGG-----LINIVTKKG---QEGKQVEL-----QIGGKTGFNSHNDHDE 173
Qy 102 NKTACMYGGVTLHDNNRLTEEEKVPTNL-----WIDGKQTTVPIDKVKTS---KKEVT 151
Db 174 NISAMSGG-----TERAFGRFSVSYORYGYMDGKGNVILIDNTQTGLQYSNRUD 224
Qy 152 V-----QELDLQARHY---LHGKFLGY-----NSDSFGG 177
Db 225 VMGTGTLNIDENQQLLTQYFNSESDGKHGLYLQGNFSAVTGTQASNSAALNSDRIPG 284
Qy 178 KVQRLIVFHSSEGSTVSYDLFDAQGYPTDLLRIY-----RDNK--TINSENHLIDLY 229
Db 285 -TERHLINLQYSNTDFWQDGLV-AQVYRDBSLTFYPPPTLKDGVSTIGASQKQTDYF 341

RESULT 92
DB3845
hypothetical protein BH1564 [imported] - Bacillus halodurans (strain C-125)
C:Species: Bacillus halodurans
C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C:Accession: DB3845
R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hiran
Nucleic Acids Res. 28, 4317-4331, 2000
A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A:Reference number: AB83650; MUID:20512582; PMID:11058132
A:Accession: DB3845
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-520 <STO>
C:Cross-references: UNIPROT:Q9KCK7; GB:AP001512; GB:BA000004; NID:g10174030; PIDN:BA052
A:Experimental source: strain C-125
C:Genetics:
A:Gene: BH1564

Query Match 6.6%; Score 82; DB 2; Length 520;
Best Local Similarity 27.5%; Pred. No. 60;
Matches 46; Conservative 23; Mismatches 58; Indels 40; Gaps 11;
Qy 48 LENTLLFKGFTTGH-----WTN---DLLVDLGSKDAT-----NKKY 81
Db 85 IESTLITGSLPDEHKVPVGLVWYHABEDRLVDYGSTPETYMKLGLNRLVFLDLSLNNRHL 144
Qy 82 GKKV-DLYGAYGYQCAGTTPNKTACMYGGVTLHDNNRLTEEEKVPTNLWDGK--QTTV 138
Db 145 SKDVPPTIHEILDQSQNSTGSVN--ALVYRGNTSHKVN-LPE----PFDTMQQOPPETKG 197
Qy 139 P-IDKVKTSKEVTQVQELDLQARHYLHGKFLGYNDSFGKQVQGLI 184
Db 198 PLLSGFTIIEPKVIQAKELDDHFL-DLYGL--NDSYGTAVVRTL 241

RESULT 93
S55243
ubiquitin-like protein 8 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 16-Aug-2004
C:Accession: S55243; S61068
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
Genetics 139, 921-939, 1995
A:Title: Structure and evolution of genes encoding polyubiquitin and ubiquitin-like prote
A:Reference number: S55242; MUID:95229071; PMID:7713442
A:Accession: S55243
A:Status: nucleic acid sequence not shown

A:Molecule type: DNA
A:Residues: 1-631 <CAL>
A:Cross-references: UNIPROT:Q39256; EMBL:L05917
A:Experimental source: ecotype Columbia
R:Callis, J.; Carpenter, T.; Sun, C.W.; Vierstra, R.D.
submitted to the EMBL Data Library, June 1995
A:Reference number: S61068
A:Accession: S61068
A:Molecule type: DNA
A:Residues: 1-341, 'E', 343-631 <CAW>
A:Cross-references: EMBL:L05917; NID:9870793; PIDN:AAA68879.1; PID:9870794
C:Superfamily: ubiquitin homology
F:3-78/Domain: ubiquitin homology <UBH1>
F:79-154/Domain: ubiquitin homology <UBH2>
F:155-237/Domain: ubiquitin homology <UBH3>
F:238-318/Domain: ubiquitin homology <UBH4>
F:319-392/Domain: ubiquitin homology <UBH5>
F:393-468/Domain: ubiquitin homology <UBH6>
F:469-551/Domain: ubiquitin homology <UBH7>
F:552-627/Domain: ubiquitin homology <UBH8>
Query Match 6.6%; Score 82; DB 2; Length 631;
Best Local Similarity 21.0%; Pred. No. 77;
Matches 64; Conservative 47; Mismatches 102; Indels 92; Gaps 17;
Qy 2 EKSEINEKDLRKSELOQNALSNLROIYYNEKAITE-NKESDDQFLEN-----TLIF 54
Db 177 ESSDTI--ENVKAKIQREGLRPHQRILFGEELFTEDNRLADYGINRSTLCIALRL 234
Qy 55 KG-----FFTGHPWYNLLVDLGSKDATNKYKG-----KVDLYGAYY-GY 94
Db 235 RGDWYIFVKNLPYNSFTG---ENFILEVSSDTIDNVKAKLQDKERIPMDLHRLIFAGK 290
Qy 95 QCAGGTNKTACMG---GVTLHNNR-----LTEEKVPINLWIDGKQTTVPI 140
Db 291 PLEGG---RTLAHYNIQKSGTLYLTPRCGMQIFVKTLTRK---INLEVESWDT--I 341
Qy 141 DKVKTS-----KKEVTVQELDLQARHYLHGKFGI-YNSDSFG 176
Db 342 DNVKAMVDKREGIQPNQLRLIFLGKELDKGCTLADYSIQKSTLHLVLGMQIFVKLFG 401
Qy 177 GKVGRLIVFHSSEGSTVSYDLFDAQGYPTTLRIYR-----DNKTY-----NSNLH 225
Db 402 GKIIIT-LEVLSSDTIKSVKAKIQKVGSPPPQIILLFRGGQLQDGRTLGDYNIIRNESTLH 460
Qy 226 IDLYL 230
Db 461 LFFHI 465
RESULT 94
T05829
hypothetical protein T5K18.240 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Jul-2004
C:Accession: T05829
R:Bevan, M.; Van Der Schueren, J.; Chuang, Y.J.; Voet, M.; Robben, J.; Voickaert, G.; Ba
submitted to the Protein Sequence Database, April 1998
A:Reference number: Z15453
A:Accession: T05829
A:Molecule type: DNA
A:Residues: 1-756 <BEV>
A:Cross-references: UNIPROT:O49464; EMBL:AL022580
A:Experimental source: cultivar Columbia; BAC clone T5K18
C:Genetics:
A:Map position: 4
A:Introns: 494/1
A:Note: T5K18.240
Query Match 6.6%; Score 82; DB 2; Length 756;
Best Local Similarity 22.8%; Pred. No. 96;
Matches 66; Conservative 28; Mismatches 96; Indels 100; Gaps 11;

Qy 26 LRQIYYNEK-----AITENKESDDQFL-----ENT----- 51
Db 289 LRQYQIPEKRVHVLGVNDENGFTSDKLRTLTFRSKLGPENSAIVLGAAGRLVXDKG 348
Qy 52 --LLFKGFFTGHPWYNLL-LVDLGSKDATNKYK--GKKVDLYGAYYGYQCAGGTPNKTAC 106
Db 349 HPLLFEAFAKIIQIYTSNVYLVVAGSGPWEQRYKELGKVSILGSL-----NPNELKG 400
Qy 107 MYGGVTLHNNRLTEE-----KKVPINLWIDGKQTTV-----PIDKV 143
Db 401 FYNGIDLVFNPTLRPOGLDITLMEAMUSGKPVWASRYASIKRTIIVNDEFGFMFAPNVEA 460
Qy 144 KTSKKEVTVOE---LDLQARHYLHGKFGLYNSDSFGKQVQRL----- 183
Db 461 LTAVMEVAVAEGERLAERGR-----KCEYAAEMFTAKSLRTLQLGSSSTFFKIPTWEK 515
Qy 184 -----IVFHSSEGSTVSYDLFDAQGYPTTLRIYRDNKNTINSENHLIDL 228
Db 516 DNVLYLVSHSSCDGLVCLYNHDKSGYVYVNPTRWYRPLCLCDYQKLMIDL 565
RESULT 95
T28156
DNA-directed RNA polymerase homolog - malaria parasite (Plasmodium falciparum)
C:Species: Plasmodium falciparum
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C:Accession: T28156
R:Fox, B.A.; Li, W.B.; Tanaka, M.; Inselburg, J.; Bzik, D.J.
Mol. Biochem. Parasitol. 61, 37-48, 1993
A:Title: Molecular characterization of the largest subunit of plasmodium falciparum RNA I
A:Reference number: Z20478; MUID:94081864; PMID:8259131
A:Accession: T28156
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2910 <FOX>
A:Cross-references: UNIPROT:Q26008; EMBL:L11172; NID:9414321; PID:9414322; PIDN:AAA72349
C:Genetics:
A:Introns: 2840/3; 2880/1
Query Match 6.6%; Score 82; DB 2; Length 2910;
Best Local Similarity 19.7%; Pred. No. 5.2e+02;
Matches 64; Conservative 44; Mismatches 83; Indels 134; Gaps 18;
Qy 2 EKSEINEKDLRKSELOQNALSNLROIYYNEKAITE-NKESDD-----QFLENTLIF- 54
Db 1382 EKKEKEKE-----NKIANTCINCYKHNSHVDDEQNCNSSLSCYQYVVLNKLDFN 1432
Qy 55 --KGFFTG-----HPWYNLLVDLGSKD-----ATNK-YK----- 81
Db 1433 LYEKYLNGKNEEGNKHILYNNCQIDERNDFLNSVTNKLKALKEPTFFNSTSTFKKIT 1492
Qy 82 -----GKKVDLYGAYYGYQCAGGTPNKTACMYGGVTLH----- 114
Db 1493 KVIEKVLTLFAARCNRLKIYIFELFQ-----NKNIMKYFFPSLVYINIFHPDVSN 1546
Qy 115 -----DNNRLTEKKVPI-----NLWIDGKQTT---VPIDKVKTS 146
Db 1547 EIKKNVINIYFKEDESPSISNNNNNNKVEDDCNQDIKIKGQETNEFIDDEKIKTK 1606
Qy 147 KK---EVTVOEL-DLQARHYLHGKFGLYNSDSFGKQVQRLIVFHSSEGSTVSYDLFDAQ 202
Db 1607 RKCSQEKTIQEIKKYKLLKFLHFAELHKKQNY-----BEGR--GYDI-DEQ 1650
Qy 203 GQY---PDTLLRIYRDNKNTINSEN 224
Db 1651 NDYNIIDEKFMNDYNDNNN-NDNLL 1674
RESULT 96
T31076
tyrocidine synthetase 3 - Brevibacillus brevis
C:Species: Brevibacillus brevis
C:Date: 02-Sep-2000 #sequence_revision 02-Sep-2000 #text_change 04-Apr-2004

C:Accession: T31076
R:Mootz, H.D.; Marahiel, M.A.
J. Bacteriol. 179, 6843-6850, 1997
A:Title: The tyrocidine biosynthesis operon of *Bacillus brevis*: Complete nucleotide sequence
A:Reference number: Z20969; MUID:98012987; PMID:9352938
A:Accession: T31076
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Cross-references: EMBL:AF004835; NID:g2623770; PID:g2623773; PIDN:AAC45930.1
C:Genetics:
A:Gene: tycc
C:Function:
A:Pathway: tyrocidine biosynthesis
C:Keywords: carrier protein; phosphopantetheine; phosphoprotein
F:510-950/Domain: acetate-CoA ligase homology <AC11>
F:968-1036/Domain: acyl carrier protein homology <ACP1>
F:1546-1987/Domain: acetate-CoA ligase homology <AC12>
F:2005-2073/Domain: acyl carrier protein homology <ACP2>
F:2583-3025/Domain: acetate-CoA ligase homology <AC13>
F:3043-3111/Domain: acyl carrier protein homology <ACP3>
F:3621-4060/Domain: acetate-CoA ligase homology <AC14>
F:4078-4146/Domain: acyl carrier protein homology <ACP4>
F:4656-5104/Domain: acetate-CoA ligase homology <AC15>
F:5122-5190/Domain: acyl carrier protein homology <ACP5>
F:5702-6147/Domain: acetate-CoA ligase homology <AC16>
F:6165-6233/Domain: acyl carrier protein homology <ACP6>
F:1000,2037,3075,4110,5154,6197/Binding site: phosphopantetheine (Ser) (covalent) #status

Query Match 6.6%; Score 82; DB 2; Length 6486;
Best Local Similarity 20.2%; Pred. No. 1.4e+03;
Matches 50; Conservative 43; Mismatches 79; Indels 76; Gaps 12;
QY 16 SELQNALSLRQIY-----YNEKAITENKESDDQFLENTLLFKGFFTG--PMY 64
DB 789 ASMQPVPVGSLEMYIAGDVAKGYFNRELTKEFPIDNFRPGTKMYR---TGDLAKWL 845
QY 65 NDLLVD-LGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTEEK 123
DB 846 PGNMEYAGRMQYQVKIRHREM-----GEI-----ETRLTQHE 880
QY 124 KVPINLWIDGKQTTVPIDKVKT-----SKKEVTVOELDQARHYLHGKFGLYNSD 173
DB 881 AV-----KEAVIVKEDSQNVLYAYLVSERELTVAEI-----REFLGRTPSYMP 928
QY 174 SP-----GGKVGRLVFSHSGSTVSVDLFDFA-QGYPTLLRIYRDNKTINS 221
DB 929 SPFFRLAEIPLTANGKVERKKL--PKPAGAVVTGTAYAAPQNEIEAKLAEIQQVVLGISQ 986
QY 222 ENLHIDLY 229
DB 987 VGIHDDFF 994

RESULT 97
exotoxin 8 [imported] - *Staphylococcus aureus* (strain N315)
C:Species: *Staphylococcus aureus*
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: A89807
R:Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mizukami-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hatcori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*.
A:Reference number: A89758; MUID:21311952; PMID:11418146
A:Accession: A89807
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-356 <KUR>
A:Cross-references: UNIPROT:Q99WH9; GB:BA000018; PID:g13700314; PIDN:BAB41612.1; GSPDB:G
A:Experimental source: strain N315
C:Genetics:

A:Gene: set8

Query Match 6.6%; Score 81.5; DB 2; Length 356;
Best Local Similarity 20.0%; Pred. No. 41;
Matches 27; Conservative 31; Mismatches 48; Indels 29; Gaps 3;

QY 64 YNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLTEEK 123
DB 225 YNDIDVFIVLED--NKYQLKKYSV-----GGITKTNKKVDHKA 261
QY 124 KVPINLWIDGKQTTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKVGQRL 183
DB 262 ELSVTKKDNQGMISRDVSEYMITKEISLSEKELDFKLRLQLEKHNLY-----GNMGST 315
QY 184 IVFHSSEGSTVSVDL 198
DB 316 IVIKMNGGKVTTEL 330

RESULT 98

A40457
replication protein A1 - human
N:Alternate names: replication protein A 70K chain
C:Species: *Homo sapiens* (man)
C:Date: 28-Feb-1992 #sequence_revision 27-Oct-1995 #text_change 09-Jul-2004
C:Accession: A40457; A44501
R:Erddile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 266, 12090-12098, 1991
A:Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subunit
A:Reference number: A40457; MUID:91268092; PMID:2050703
A:Accession: A40457
A:Molecule type: mRNA
A:Residues: 1-216, 'A', 218-616 <ERD>
A:Cross-references: UNIPROT:P27694; GB:M63488
A:Note: parts of the sequence determined by protein sequencing
A:Note: this sequence has been corrected in reference A44501
R:Erddile, L.F.; Heyer, W.D.; Kolodner, R.; Kelly, T.J.
J. Biol. Chem. 268, 2268, 1993
A:Title: Characterization of a cDNA encoding the 70-kDa single-stranded DNA-binding subunit
A:Reference number: A44501; MUID:93131993; PMID:8420996
A:Accession: A44501
A:Molecule type: mRNA
A:Residues: 217 <ER2>
A:Cross-references: GB:M63488
A:Note: sequence correction
C:Genetics:
A:Gene: GDB:RPAL
A:Cross-references: GDB:138362; OMIM:179835
A:Map position: 17p13.3-17p13.3
C:Complex: Replication protein A is a trimer of 70K (A1), 32K (A2), and 14K (A3) chains.
C:Function:
A:Description: probable eukaryotic equivalent of prokaryotic single-stranded DNA-binding
probably also has a role in the elongation stage of DNA replication
A:Pathway: DNA replication initiation
A:Note: the single-stranded DNA-binding activity resides in the A1 protein
C:Superfamily: replication protein A1
C:Keywords: DNA replication initiation; single-stranded DNA binding; trimer; zinc finger
P:481-503/Region: zinc finger CCCC motif

Query Match 6.6%; Score 81.5; DB 1; Length 616;
Best Local Similarity 25.1%; Pred. No. 82;
Matches 56; Conservative 25; Mismatches 57; Indels 85; Gaps 15;

QY 23 LSNLRQIYVY-----NEKAITENKES-----DDQFLENTLLFKGFFTG 60
DB 248 LIEVANKVYFSGTKLIANKQFTAVKNYEMTFNNETSNVMPCEDDHLP-TVQFD--FTG 304
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDLYGAYGYQCAGGTENKTKACMYGGVTLHDNNRLT 120
DB 305 -----ID-----DLENKSKSLVDIIIGICKSYEDA-----TKITVRSNNREV 341
QY 121 EEKKVPINLWIDGKQTTVP-----DKVTSKKEVTVOELDQARHYLHGKFGLYNSDSF 175

Db 342 AKRNIYL-MDTSGKVVTATLWGEDADKPDGSRQPVLAIK-----GARVSD-F 386
Qy 176 GKGQVQGLIVFHSSEGSTV-----SYDL---FDAQGQYPD 207
Db 387 GG---RSLSVLSS---STIIANPDIPAYKURGFDAEGQALD 423
RESULT 99
G90571
hypothetical protein MYPU 4790 [imported] - Mycoplasma pulmonis (strain UAB CTIP)
C:Species: Mycoplasma pulmonis
C:Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C:Accession: G90571
R:Chambaud, I.; Heilig, R.; Ferris, S.; Barbe, V.; Samson, D.; Galissou, F.; Moszer, I.;
Nucleic Acids Res. 29, 2145-2153, 2001
A:Title: The complete genome sequence of the murine respiratory pathogen Mycoplasma pulm
A:Reference number: A99512; MUID:21267165; PMID:11353084
A:Accession: G90571
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-804 <KUR>
A:Cross-references: UNIPROT:Q98087; GB:AL445566; PID:gi4089893; PIDN:CAC13652.1; GSPDB:C
A:Experimental source: strain UAB CTIP
C:Genetics:
A:Gene: MYPU 4790
A:Genetic code: SGC3
Query Match 6.6%; Score 81.5; DB 2; Length 804;
Best Local Similarity 18.5%; Pred. No. 1.1e+02;
Matches 47; Conservative 42; Mismatches 74; Indels 91; Gaps 9;
Qy 3 KSEINEKDLRKSELRNALSRLR-----QIYYNEKA-----ITENKE 42
Db 501 KNYEQDNKDIRKISDDKLYNKIDIRLFLELQWAKTKKIFVGNIEEINNWLKPFIDQNFK 560
Qy 43 SDDQFLENTLLFGKFTTGHPPWYNLLVDLGSKDNTNKKY----- 81
Db 561 KD-----ENISIDFGWYVLFKDKNQKFEIENKLEKNEYKEVVEYQIFRSKNLPFYSEIF 616
Qy 82 ----GKKVDLYGAYGYQCAGGTGPNKTCMYGGVTLHDNNRLTEKKVPINLWIDGKQTT 137
Db 617 LEKSNKIDFNKAYV-----QITKKDKNQKDD-----IQLESKNET 658
Qy 138 VPIDKVTTSKEVTQELDLQARHYLGKFLGYNDSFGGKVGQGLIVFHSSEGSTVSYD 197
Db 659 SFLEIKKIFKQKHKEIWSKNIPHQ--CI-----GFDYIHNDKHT----- 700
Qy 198 LFDAQGQYVPTLLR 211
Db 701 -----SPPDFIIR 708
RESULT 100
G88637
protein F53H1.4 [imported] - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: G88637
R:anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A:Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A:Reference number: A75000; MUID:99069613; PMID:9851916
A:Note: see websites genome.wustl.edu/gsc/C_elegans/ and www.sanger.ac.uk/projects/C_ele
A:Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A:Accession: G88637
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1378 <STO>
A:Cross-references: UNIPROT:O45075; GB:chr_IV; PIDN:AAC02578.1; PID:g2854159; GSPDB:GN00
C:Genetics:
A:Gene: F53H1.4
A:Map position: 4

Query Match 6.6%; Score 81.5; DB 2; Length 1378;
Best Local Similarity 20.1%; Pred. No. 2.2e+02;
Matches 54; Conservative 41; Mismatches 100; Indels 73; Gaps 11;
Qy 2 EKSEINEKDLRKSELRNALSRLRQIYYNEKAI---TENKESD-----DQFLENTLLFK 55
Db 253 KKKQEQBEKKQKKBEKAKKLKEKEEKLKEKEKAKAKAEKKEKNGTMDKFLKKD----- 308
Qy 56 GFFTGHF-----WYNDLLVDLGSKDNTNKKYKGVLDLYGAYGYQCAGGTENK 103
Db 309 ---TGSFSSKNAPLFSFSKW-GEKRIAGVKKMEDANKRRDLEY-----N 350
Qy 104 TACMYGGVTLHDNNRLTEEK---KVPINLWIDGKQTTVPIDKVKTSKEVTQVQELDLQAR 160
Db 351 EACSWCEKNLSGNQSTFENPIKFSYQKLVDAKADRAHMKGMKWAQKAEFKAEWS-EKR 409
Qy 161 HYLHCKF-----GLYNSDSFGGKVGQGLIVFHSSEGSTVSYDLFDAQ----- 202
Db 410 KELYQKFEPIKAKWFNED-----IALDDLLVTCENLELLELDKRVNCDDELLKCLE 459
Qy 203 -GOYVPTLLRIYRDNKTINGENLHIDLY 229
Db 460 ISQFFVSMRKILLWNENITAEQLRDDLH 487
Search completed: July 26, 2005, 11:08:47
Job time : 25 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: July 26, 2005, 10:59:53 ; Search time 173 Seconds
(without alignments)
689.679 Million cell updates/sec

Title: US-09-900-766-7
Perfect score: 1238
Sequence: 1 SEKSEINKEKDLRKKESELR.....RDNKTINSEMLHIDLYLTT 233

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 200 summaries

Database :
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1238	100.0	257	1	ETXG_STPAU
2	1023	82.6	257	1	ETXG_STPAU
3	1023	82.6	257	2	Q6G7Y7
4	1023	82.6	257	2	Q931M4
5	1013	81.8	257	2	Q6GFA8
6	994	80.3	257	2	Q99SU3
7	971	78.4	219	2	Q6XZS9
8	837	67.6	258	2	Q6LS7
9	830	67.0	258	2	Q6S217
10	825	66.6	154	2	Q6R2G0
11	663	53.6	258	1	ETXD_STPAU
12	496	40.1	152	2	Q6R2F9
13	490.5	39.6	229	2	Q6NW97
14	490.5	39.6	229	2	Q6G8W7
15	461.5	37.3	258	2	Q7A2G6
16	461.5	37.3	258	2	Q7A4X1
17	461.5	37.3	258	2	Q9E2M4
18	446.5	36.1	251	2	Q6YCN3
19	446.5	36.1	251	2	Q6GFM1
20	414	33.4	254	2	Q6GFM7
21	387.5	31.3	260	2	Q99T46
22	387.5	31.3	260	2	Q7A4W6
23	387.5	31.3	261	2	Q9E2M8
24	381	30.8	179	2	Q52075
25	366	29.6	217	2	Q6R876
26	366	29.6	241	1	ETXG_STPAU
27	366	29.6	241	2	Q6VAM8
28	366	29.6	241	2	Q6GDA5
29	348.5	28.2	242	2	Q6YCN5
30	348.5	28.2	242	2	Q6GFM9
31	341.5	27.6	225	2	Q8VWV1

32	339.5	27.4	242	2	Q8S383
33	339.5	27.4	242	2	Q7A2Q5
34	339.5	27.4	242	2	Q7A4W8
35	337	27.2	240	2	Q7A2N9
36	337	27.2	240	2	Q7A4K9
37	337	27.2	240	2	Q9F0L7
38	336	27.1	240	2	Q8NXJ5
39	335.5	27.1	218	2	Q8RR75
40	335.5	27.1	225	2	Q9L921
41	334.5	27.0	225	2	Q99Z21
42	320	25.8	239	2	Q99T47
43	320	25.8	239	2	Q7A4W7
44	319.5	25.8	242	2	Q8NVW3
45	319.5	25.8	242	2	Q6G7U1
46	318.5	25.7	256	2	Q8VLM7
47	316.5	25.6	242	2	Q93CC6
48	316	25.5	239	2	Q9E2M7
49	312	25.2	86	2	Q711S9
50	310	25.0	242	2	Q8NVW2
51	310	25.0	242	2	Q6G7U0
52	309	25.0	163	2	Q6R2F8
53	309	25.0	242	2	Q54476
54	309	25.0	242	2	Q93CC5
55	302	24.4	239	2	Q6GFM8
56	300.5	24.3	266	1	ETXG_STPAU
57	298	24.1	261	2	Q6YCN4
58	298	24.1	261	2	Q6GFM0
59	295.5	23.9	251	1	SPER_STRP8
60	295.5	23.9	251	1	SPER_STRP7
61	295	23.8	177	2	Q6R1Y7
62	294.5	23.8	251	2	Q8K6K5
63	291.5	23.5	261	2	Q6XXM3
64	290.5	23.5	261	2	Q6XXM5
65	289.5	23.3	207	2	Q7X0E8
66	288.5	23.3	261	2	Q6XXM4
67	287.5	23.2	218	2	Q7X0E7
68	286.5	23.1	239	2	Q06531
69	285.5	23.1	239	2	Q06532
70	285.5	23.1	239	2	Q06533
71	285.5	23.1	266	1	ETC3_STPAU
72	284.5	23.0	239	2	Q06535
73	283.5	22.9	239	2	Q05157
74	283.5	22.9	266	2	Q8NXJ6
75	282.5	22.8	239	2	Q06533
76	281.5	22.7	266	1	ETC2_STPAU
77	280.5	22.7	207	2	Q7X0E6
78	280.5	22.7	222	2	Q6XZB6
79	280.5	22.7	239	2	Q6S749
80	279.5	22.6	236	2	Q54696
81	279.5	22.6	271	2	Q9F0L6
82	278.5	22.5	236	2	P97163
83	278.5	22.5	239	2	Q53678
84	277.5	22.4	222	2	Q938P4
85	277.5	22.4	222	2	Q9S524
86	277.5	22.4	234	2	Q9R5X4
87	277.5	22.4	236	2	Q54779
88	276.5	22.3	222	2	Q9R931
89	276.5	22.3	236	2	Q57453
90	272.5	22.0	239	2	Q06534
91	269.5	21.8	260	2	Q54738
92	267.5	21.6	260	2	Q54738
93	267.5	21.6	260	2	Q79X14
94	267.5	21.6	260	2	Q54739
95	266.5	21.5	266	1	ETC1_STPAU
96	264.5	21.4	258	2	Q6GFM2
97	262.5	21.2	222	2	Q6XZB7
98	259.5	21.0	264	2	Q764P6
99	256.5	20.7	209	2	Q9R005
100	255	20.7	233	2	Q8R877
101	255.5	20.6	258	1	ETXG_STPAU
102	255.5	20.6	258	1	Q9E2M3
103	255.5	20.6	258	1	Q9E2M3
104	253	20.4	209	2	Q9LAD8

Q8S383	staphylococ
Q7A2Q5	staphylococ
Q7A4W8	staphylococ
Q7A2N9	staphylococ
Q7A4K9	staphylococ
Q9F0L7	staphylococ
Q8NXJ5	staphylococ
Q8R75	staphylococ
Q9L921	staphylococ
Q99Z21	staphylococ
Q99T47	staphylococ
Q7A4W7	staphylococ
Q8NVW3	staphylococ
Q6G7U1	staphylococ
Q8VLM7	staphylococ
Q93CC6	staphylococ
Q9E2M7	staphylococ
Q711S9	staphylococ
Q8NVW2	staphylococ
Q6G7U0	staphylococ
Q6R2F8	staphylococ
Q54476	staphylococ
Q93CC5	staphylococ
Q6GFM8	staphylococ
ETXG_STPAU	staphylococ
Q6YCN4	staphylococ
Q6GFM0	staphylococ
P01552	staphylococ
Q6S749	staphylococ
Q54696	staphylococ
Q9F0L6	staphylococ
P97163	staphylococ
Q53678	staphylococ
Q938P4	staphylococ
Q9S524	staphylococ
Q9R5X4	staphylococ
Q54779	staphylococ
Q9R931	staphylococ
Q57453	staphylococ
Q06534	staphylococ
Q54738	staphylococ
Q54738	staphylococ
Q79X14	staphylococ
Q54739	staphylococ
P01553	staphylococ
Q6GFM2	staphylococ
Q9E2M3	staphylococ
Q764P6	staphylococ
Q9R005	staphylococ
Q8R877	staphylococ
ETXG_STPAU	staphylococ
Q9E2M3	staphylococ
Q9LAD8	staphylococ

105	253	20.4	209	2	Q91A60	Q91A60 streptococc
106	251.5	20.3	259	2	Q76LS8	Q76LS8 staphylococc
107	251	20.3	209	2	Q91AC6	Q91AC6 streptococc
108	251	20.3	209	2	Q91AD1	Q91AD1 streptococc
109	249	20.1	209	2	Q91AC4	Q91AC4 streptococc
110	249	20.1	209	2	Q91AE1	Q91AE1 streptococc
111	249	20.1	233	2	Q76M7	Q76M7 streptococc
112	247.5	20.0	220	2	Q79A00	Q79A00 streptococc
113	247	20.0	209	2	Q91AC5	Q91AC5 streptococc
114	246	19.9	209	2	Q91AC7	Q91AC7 streptococc
115	245.5	19.8	159	2	Q6R2G1	Q6R2G1 staphylococc
116	245.5	19.8	214	2	Q6XZ88	Q6XZ88 staphylococc
117	244	19.7	209	2	Q91AD2	Q91AD2 streptococc
118	244	19.7	209	2	Q91AD6	Q91AD6 streptococc
119	243	19.6	207	2	Q7WY99	Q7WY99 streptococc
120	243	19.6	233	2	Q6VBI7	Q6VBI7 streptococc
121	242	19.5	209	2	Q91AD9	Q91AD9 streptococc
122	242	19.5	233	2	Q8N289	Q8N289 streptococc
123	241	19.5	209	2	Q91AC3	Q91AC3 streptococc
124	240	19.4	209	2	Q91AD4	Q91AD4 streptococc
125	239	19.3	209	2	Q91AC3	Q91AC3 streptococc
126	239	19.3	209	2	Q91AC8	Q91AC8 streptococc
127	238	19.2	256	2	Q9S1H8	Q9S1H8 streptococc
128	237.5	19.2	180	2	Q6DTL6	Q6DTL6 streptococc
129	237	19.1	209	2	Q91AD5	Q91AD5 streptococc
130	234	18.9	209	2	Q91AD7	Q91AD7 streptococc
131	233	18.8	209	2	Q91AD3	Q91AD3 streptococc
132	232	18.7	233	2	Q99XW1	Q99XW1 streptococc
133	231.5	18.7	180	2	Q6DTL4	Q6DTL4 streptococc
134	231	18.7	209	2	Q91AD0	Q91AD0 streptococc
135	228	18.4	183	2	Q6DTL3	Q6DTL3 streptococc
136	227	18.3	259	2	Q936G4	Q936G4 staphylococc
137	224	18.1	183	2	Q6DTL5	Q6DTL5 streptococc
138	220.5	17.8	131	2	Q7CEP2	Q7CEP2 streptococc
139	220	17.8	234	2	Q8K807	Q8K807 streptococc
140	218	17.6	183	2	Q6DTL1	Q6DTL1 streptococc
141	217	17.5	234	1	SEPG_STRPY	SEPG_STRPY
142	217	17.5	240	2	Q8P2R5	Q8P2R5 streptococc
143	216	17.4	210	2	Q9K2G9	Q9K2G9 streptococc
144	214	17.3	234	2	Q76FM2	Q76FM2 streptococc
145	213	17.2	234	2	Q76FM3	Q76FM3 streptococc
146	208	16.8	234	2	Q76FM0	Q76FM0 streptococc
147	205	16.6	234	2	Q76FM5	Q76FM5 streptococc
148	203	16.4	234	2	Q76FM7	Q76FM7 streptococc
149	201	16.2	157	2	Q99TP7	Q99TP7 staphylococc
150	201	16.2	157	2	Q7AS47	Q7AS47 staphylococc
151	199	16.1	234	2	Q76FM6	Q76FM6 streptococc
152	199	16.1	236	2	Q91920	Q91920 streptococc
153	198	16.0	234	2	Q76FM9	Q76FM9 streptococc
154	197	15.9	136	2	Q99T49	Q99T49 staphylococc
155	197	15.9	136	2	Q7A4X0	Q7A4X0 staphylococc
156	197	15.9	195	2	Q6YCN2	Q6YCN2 staphylococc
157	197	15.9	234	2	Q93RR9	Q93RR9 streptococc
158	197	15.9	234	2	Q8G9K7	Q8G9K7 streptococc
159	197	15.9	236	1	SEPH_STRPY	SEPH_STRPY
160	193	15.6	232	2	Q7BAE3	Q7BAE3 streptococc
161	187	15.1	256	2	Q9S1H9	Q9S1H9 streptococc
162	187	15.1	256	2	Q9X9R8	Q9X9R8 streptococc
163	185	14.9	235	2	Q8NKK2	Q8NKK2 streptococc
164	180	14.5	235	1	SPCC_STRPY	SPCC_STRPY
165	168	13.6	206	2	Q6LDJ6	Q6LDJ6 streptococc
166	163	13.2	206	2	Q54512	Q54512 streptococc
167	160.5	13.0	108	2	Q9EZM5	Q9EZM5 staphylococc
168	147	11.9	167	2	Q7X0E4	Q7X0E4 staphylococc
169	144	11.6	62	2	Q99TP8	Q99TP8 staphylococc
170	144	11.6	62	2	Q7AS48	Q7AS48 staphylococc
171	138	11.1	167	2	Q7X0E5	Q7X0E5 staphylococc
172	135	10.9	259	2	Q70EW3	Q70EW3 streptococc
173	135	10.8	262	2	Q8P0S0	Q8P0S0 streptococc
174	134	10.8	227	2	Q849U3	Q849U3 streptococc
175	134	10.8	262	2	Q70EW2	Q70EW2 streptococc
176	133	10.7	167	2	Q7W859	Q7W859 staphylococc
177	130	10.5	259	2	Q938J1	Q938J1 temperate p

ALIGNMENTS

178	127.5	10.3	62	2	Q8N1V9	Q8N1V9 staphylococc
179	126	10.2	209	2	Q879B0	Q879B0 streptococc
180	126	10.2	233	2	Q849U4	Q849U4 streptococc
181	123	9.9	132	2	Q9EZM6	Q9EZM6 staphylococc
182	123	9.9	133	2	Q99T48	Q99T48 staphylococc
183	123	9.9	133	2	Q7A4W9	Q7A4W9 staphylococc
184	122	9.9	156	2	Q71US9	Q71US9 streptococc
185	118.5	9.6	156	2	Q7BR4	Q7BR4 streptococc
186	116.5	9.4	231	2	Q9RN32	Q9RN32 staphylococc
187	116	9.4	231	2	Q9ZFS5	Q9ZFS5 staphylococc
188	116	9.4	231	2	Q6GJP2	Q6GJP2 staphylococc
189	114.5	9.2	231	2	Q8N1V4	Q8N1V4 staphylococc
190	114.5	9.2	231	2	Q6GCS8	Q6GCS8 staphylococc
191	114	9.2	231	2	Q9RN3	Q9RN3 staphylococc
192	113.5	9.2	1400	2	Q66AL1	Q66AL1 dictyosteli
193	113	9.1	232	2	Q99WH4	Q99WH4 staphylococc
194	113	9.1	232	2	Q7A7H2	Q7A7H2 staphylococc
195	112.5	9.1	237	2	Q8P0R9	Q8P0R9 streptococc
196	111.5	9.0	443	2	Q8CM25	Q8CM25 staphylococc
197	109	8.8	232	2	Q9ZFS4	Q9ZFS4 staphylococc
198	109	8.8	232	2	Q8N1V6	Q8N1V6 staphylococc
199	109	8.8	232	2	Q6GCS6	Q6GCS6 staphylococc
200	109	8.8	232	2	Q6GJP1	Q6GJP1 staphylococc

RESULT 1

ID EXTX STRAU STANDARD; PRT; 257 AA.

AC P12993;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enterotoxin type E precursor (SEB).
 GN Name=entE;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-74.
 RC STRAIN=MUR265;
 RX MEDLINE=88257005; PubMed=3384800;
 RA "Couch J.L., Solitis M.T., Betley M.J.;
 "Cloning and nucleotide sequence of the type E staphylococcal
 RT enterotoxin gene.";
 RL J. Bacteriol. 170:2954-2960 (1988).
 RN [2]
 RP 3D-STRUCTURE MODELING.
 RX MEDLINE=96022987; PubMed=7552730;
 RA "Swaminathan S., Furey W.F. Jr., Pletcher J., Sax M.;
 "Residues defining V beta specificity in staphylococcal
 RT enterotoxins.";
 RL Nat. Struct. Biol. 2:680-686 (1995).
 CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
 staphylococcal food poisoning syndrome. The illness characterized
 by high fever, hypotension, diarrhea, shock, and in some cases
 death.
 CC -1- CORPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
 for the toxin interaction with MHC class II (by similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
 family.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use by non-profit institutions as long as its content is in no way
 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)
 or send an email to license@ebi.ac.uk.
 CC -----

```

DR EMBL: M21319; AAA26617.1;
DR PIR: A28179; A28179.28-257.
DR PDB: 1SBE; Model: @28-257.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact1_tox.
DR InterPro: IPR01050; Pectin_lyas_1ike.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Scap_stp_tox_1.
DR Pfam: PF01123; Scap_stp_toxin; 1.
DR PRINTS: PR00279; BACTR1TOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR 3D-structure; Direct protein sequencing; Enterotoxin; Metal-binding;
KM Signal; Superaantigen; Toxin; Zinc.
FT SIGNAL 1 27
FT CHAIN 28 257 Enterotoxin type E.
FT METAL 211 211 Zinc (By similarity).
FT METAL 249 249 Zinc (By similarity).
FT METAL 251 251 Zinc (By similarity).
FT HELIX 33 35
FT STRAND 42 42
FT STRAND 46 47
FT STRAND 48 51
FT HELIX 52 54
FT STRAND 59 64
FT STRAND 66 67
FT STRAND 69 69
FT STRAND 73 74
FT STRAND 75 79
FT TURIN 83 84
FT STRAND 90 94
FT HELIX 98 104
FT TURIN 105 106
FT STRAND 109 113
FT STRAND 115 116
FT TURIN 118 119
FT STRAND 128 132
FT STRAND 135 137
FT STRAND 139 140
FT STRAND 142 142
FT STRAND 152 152
FT STRAND 154 155
FT TURIN 156 157
FT STRAND 163 163
FT STRAND 171 171
FT STRAND 173 175
FT HELIX 176 190
FT TURIN 191 191
FT STRAND 203 211
FT STRAND 219 221
FT STRAND 227 227
FT HELIX 234 239
FT STRAND 242 244
FT TURIN 245 247
FT STRAND 249 257
SQ SEQUENCE 257 AA; 29358 MW; 27EDA9AB97770CE3 CRC64;

Query Match 100.0%; Score 1238; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 6; 6e-94;
Matches 233; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Db 145 EKKVPINLMIDGKQTVPIIDKVTSKKEVTVOEJLDQAHYHKGKFGVNSDSFGKQV 204
Qy 181 RGLIVFHSSEGSTVSVDLFDAGQVPTLIRKNTKINSNLIIDLYLT 233
Db 205 RGLIVFHSSEGSTVSVDLFDAGQVPTLIRKNTKINSNLIIDLYLT 257

RESULT 2
ID EXTRA STRAW STANDARD; PRT; 257 AA.
AC P13163;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterotoxin type A precursor (SEA).
GN Name=entA; OrderedLocustNames=MM1889;
OS Staphylococcus aureus (strain MW2), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwano N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
acquired MRSA.";
RL Lancet 359:1819-1827(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FR1337;
RX MEDLINE=88086892; PubMed=3335483;
RA Beley M.J., Mekalanos J.J.;
RT "Nucleotide sequence of the type A staphylococcal enterotoxin gene.";
RL J. Bacteriol. 170:34-41(1988).
RN [3]
RP SEQUENCE OF 25-257.
RX MEDLINE=87222293; PubMed=3584106;
RA Huang I.-Y., Hughes J.L., Bergdoll M.S., Schantz E.J.;
RT "Complete amino acid sequence of staphylococcal enterotoxin A.";
RL J. Biol. Chem. 262:7006-7013(1987).
RN [4]
RP X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
RX MEDLINE=95354648; PubMed=7628431;
RA Schad E.M., Zaitseva I., Zaitsev V.N., Dohlesten M., Kalland T.,
RA Schlievert P.M., Ohlendorf D.H., Svensson L.A.;
RT "Crystal structure of the superantigen staphylococcal enterotoxin type
A.";
RL EMBO J. 14:3292-3301(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
RX MEDLINE=97113025; PubMed=8943278; DOI=10.1074/jbc.271.50.32212;
RA Sundstroem M., Hallen D., Svensson A., Schad E., Dohlesten M.,
RA Abrahamson L.;
RT "The Co-crystal structure of staphylococcal enterotoxin type A with
Zn2+ at 2.7-A resolution. Implications for major histocompatibility
complex class II binding.";
RL J. Biol. Chem. 271:32212-32216(1996).
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=96022987; PubMed=7552730;
RA Swaminathan S., Furey W.F., Jr., Pletcher J., Sax M.;
RT "Residues defining V beta specificity in staphylococcal
enterotoxins.";
RL Nat. Struct. Biol. 2:680-686(1995).
RN [7]
RP COMPARISON OF STRUCTURE OF SEA AND SECC.
RX MEDLINE=97334373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
RT "A structural and functional comparison of staphylococcal enterotoxins

```

RT A and C2 reveals remarkable similarity and dissimilarity.";
RL J. Mol. Biol. 269:270-280(1997).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- CORPACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBUNIT: Monomer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- MISCELLANEOUS: This toxin seems to be coded by a bacteriophage.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AP004828; BAB95754.1; -.
DR EMBL: M18970; AAA26681.1; -.
DR PIR: A28664; A28664.1; -.
DR PDB: 1DYQ; X-ray; A=24-257.
DR PDB: 1ESF; X-ray; A/B=-.
DR PDB: 1I4G; X-ray; A/B=25-257.
DR PDB: 1I4H; X-ray; A/B=25-257.
DR PDB: 1LO5; X-ray; D=25-257.
DR PDB: 1SEA; Model; @=25-257.
DR PDB: 1SXT; X-ray; A/B=25-257.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; BactI tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF02876; Staph_Strep_toxin; 1.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR PRINTS: PR00279; BACTRILTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR 3D-structure: Complete proteome; Direct protein sequencing;
KW Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24
FT CHAIN 25 257 Enterotoxin type A.
FT DISULFID 120 130
FT METAL 211 211 Zinc.
FT METAL 249 249 Zinc.
FT METAL 251 251 Zinc.
FT CONFLICT 242 242 T -> S (in Ref. 3).
FT HELIX 33 35
FT HELIX 39 41
FT HELIX 41 45
FT TURN 44 45
FT HELIX 46 55
FT STRAND 59 65
FT STRAND 75 78
FT TURN 79 80
FT STRAND 90 94
FT STRAND 98 104
FT TURN 105 106
FT STRAND 109 114
FT STRAND 116 116
FT HELIX 117 119
FT TURN 122 123
FT TURN 126 127
FT STRAND 128 132
FT STRAND 135 137
FT TURN 139 140
FT STRAND 143 148
FT STRAND 151 155
FT TURN 156 157
FT STRAND 158 160

FT TURN 164 165
FT STRAND 168 171
FT STRAND 173 175
FT HELIX 176 191
FT TURN 193 194
FT HELIX 197 199
FT TURN 200 200
FT STRAND 205 211
FT STRAND 218 221
FT TURN 222 223
FT TURN 227 228
FT TURN 230 232
FT HELIX 233 237
FT TURN 238 239
FT STRAND 242 244
FT TURN 246 247
FT STRAND 249 255
SQ SEQUENCE 257 AA; 29669 MW; ADEBFBSCA1F14677 CRC64;
Query Match 82.6%; Score 1023; DB 1; Length 257;
Best Local Similarity 82.0%; Pred. No. 3,4e-76;
Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;
QY 1 SEKSEINERKDLRKSEIQRNALNLRQIYYNEKATENKESDDQPLENTLLFKGFTG 60
DB 25 SEKSEINERKDLRKSSSEIQRTALGNLQIYYNEKAKTENKESHQFLQHTLLFKGFTD 84
QY 61 HPWYNDLLVDLGSKDATNKYKGVLDGAYYGYQACAGTPTNKTCMYGYTLHDNNELT 120
DB 85 HSWYNDLLVDLFDSDNDYDKYKGVLDGAYYGYQACAGTPTNKTCMYGYTLHDNNELT 144
QY 121 EEKVPINLWIDGKQTTYPIDRKVTSKEEVTVQSELDLQARYHLGKFLYNSDSGKGVQ 180
DB 145 EEKVPINLWIDGKQTTYPIDRKVTSKEEVTVQSELDLQARYHLGKFLYNSDSGKGVQ 204
QY 181 RGLVFFHSSEGSTVYDLFDAQGOYPTLRLIYRDNKNTINSENLHIDLYTT 233
DB 205 RGLVFFHSSTEPSVYDLFGAQGOISNTLRLIYRDNKNTINSENLHIDLYTT 257
RESULT 3
ID 06G7Y7 PRELIMINARY; PRT; 257 AA.
AC 06G7Y7
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
GN Enterotoxin type A.
OS OrderedLocustNames=SAS1872;
OS Staphylococcus aureus (strain MSS4476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN [1]
RP SEQUENCE FROM N. A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Feil E.V., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagele K.,
RA James K.D., Leonard N., Line A., Mayes R., Moule S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Stimpson M., Stevens K., Whitehead S., Barrall B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571857; CAG43678.1; -.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; BactI tox.
DR InterPro: IPR006123; Staph/Strep_toxin.

DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 29669 MW; ADBEFSECALF1677 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 257;
 Best Local Similarity 82.0%; Pred. No. 3.4e-76;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84
 QY 61 HSWYNDLVLDGSKATNKYKKVDLYGAYYGOCAGGTPNKTACMGVTLHDNNRLT 120
 DB 85 HSWYNDLVLDGSKATNKYKKVDLYGAYYGOCAGGTPNKTACMGVTLHDNNRLT 144
 QY 121 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVG 180
 DB 145 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVG 204
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLT 233
 DB 205 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLT 257

RESULT 4
 Q931M4 PRELIMINARY; PRT; 260 AA.

AC Q931M4;
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 25, Last annotation update)
 DE Enterotoxin P.
 GN Name=sep; OrderedLocustNames=SAV1948;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=158878;
 RX SEQUENCE FROM N.A.
 RC STRAIN=Mu50 / ATCC 700699;
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
 RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hoshiyama A.,
 RA Mizutani U. Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekitani K., Hiramatsu H., Kubara S., Goto S., Yabuuchi J.,
 RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 aureus."
 RT Lancet 357:1225-1240(2001).
 DR EMBL: AP003364; BAB58110.1; -.
 DR HSSP: P13163; ILO5.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 260 AA; 30016 MW; 15C2D36270FA8241 CRC64;

Query Match 82.6%; Score 1023; DB 2; Length 260;
 Best Local Similarity 82.0%; Pred. No. 3.5e-76;
 Matches 191; Conservative 17; Mismatches 25; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 28 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 87
 QY 61 HSWYNDLVLDGSKATNKYKKVDLYGAYYGOCAGGTPNKTACMGVTLHDNNRLT 120
 DB 88 HSWYNDLVLDGSKATNKYKKVDLYGAYYGOCAGGTPNKTACMGVTLHDNNRLT 147
 QY 121 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVG 180
 DB 148 EEKVPINIMIDGKQTPVIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDFGKVG 207
 QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLT 233
 DB 208 RGLIVFHSSEGSTVSYDLFDAQGYPTLLRIYRDNKTINSENHIDLYLT 260

RESULT 5
 Q6GFAB PRELIMINARY; PRT; 257 AA.

AC Q6GFAB;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Enterotoxin type A.
 GN OrderedLocustNames=SR2043;
 OS Staphylococcus aureus (strain MRSA252).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 NCBI_TaxID=282458;
 RX SEQUENCE FROM N.A.
 RP PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
 RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Feltwell T., Hance Z., Harris B., Hauser H., Holtrov S., Jagels K.,
 RA James K.D., Lennard N., Line A., Mayes R., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
 RA Spratt B.G., Parkhill J.,
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL: BX572856; CAG41028.1; -.
 DR GO: GO:000576; C:extracellular; IEA.
 DR GO: GO:0009405; P:pathogenesis; IEA.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactrl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF01123; Staph_Strep_toxin_1.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Complete proteome.
 SQ SEQUENCE 257 AA; 29674 MW; 56B0A6D952BDFED4 CRC64;

Query Match 81.8%; Score 1013; DB 2; Length 257;
 Best Local Similarity 81.5%; Pred. No. 2.3e-75;
 Matches 190; Conservative 17; Mismatches 26; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTG 60
 DB 25 SEKSEINEKDLRKSELOALNSLRQIYYNEKAITENKESDDOFLNTLLFKGFFTD 84

```
Qy 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLT 120
Db 85 HSWYNDLLVDLGSKDQIYDKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLT 144
Qy 121 EEKKVPINLWLDGKQTVPIDKVTSKKEVTVQELDLQARHHLHGKFGLYNSDSFGKRVQ 180
Db 145 EEKKVPINLWLDGKQTVPIETVKTKKNVTVQELDLQARRLOKQKLYNSDVDDGKRVQ 204
Qy 181 RGLIVFHSSEGSTVSYDLPDAQGYPTLLRIYRDNKNTINSENHIDLYLTT 233
Db 205 RGLIVFHSSTEPSVYDLPFGAQGQNSNTLLRIYRDNKNTINSENHIDLYLTS 257
```

RESULT 6

```
099SUS3 PRELIMINARY; PRT; 260 AA.
AC 099SUS3.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE Enterococin P.
GN Name=sej; OrderedLocusNames=SA1761;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=N315;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iihara J., Ito T.,
RA Kanamori M., Matsumaru H., Murakami H., Hoshino A.,
RA Mitani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL; AP003135; BAB43036.1; -.
DR PIR; C89984; C89984.
DR HSSP; P13163; ISXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29708 MW; 087C5B4EC028CFDB CRC64;
```

```
Query Match 80.3%; Score 994; DB 2; Length 260;
Best Local Similarity 79.0%; Pred. No. 8.5e-74;
Matches 184; Conservative 17; Mismatches 32; Indels 0; Gaps 0;
```

```
Qy 1 SEKSEINEKDLRKSELORNALSNLROIYYNEKAITENKESDDQFLNTLLFKGFFTG 60
Db 28 SEKSEINIGKLOKSELOSTALSNLROTYHNSAIIENKESNQFLKNTLLFNDFTG 87
Qy 61 HPWYNDLLVDLGSKDATNKKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLT 120
Db 88 HSWYNDLLVDLGSKDQIYDKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLT 147
Qy 121 EEKKVPINLWLDGKQTVPIDKVTSKKEVTVQELDLQARHHLHGKFGLYNSDSFGKRVQ 180
Db 148 EEKKVPINLWLDGKQTVPIETVKTKKNVTVQELDLQARRLOKQKLYNSDVDDGKRVQ 207
```

```
Qy 181 RGLIVFHSSEGSTVSYDLPDAQGYPTLLRIYRDNKNTINSENHIDLYLTT 233
Db 208 RGLIEFHSSESDSVGYDLPFGAQGQPTQLRIYRDNKNTIKSKNMHIDLYLTT 260
```

RESULT 7

```
06XZB9 PRELIMINARY; PRT; 219 AA.
ID 06XZB9.
AC 06XZB9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Enterococin sea variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=320E;
RX MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RA Leterre C., Perelle S., Dilaeser F., Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterococin
RT genes sea to sej of Staphylococcus aureus."
RL Mol. Cell. Probes 17:227-235(2003).
DR EMBL; AY196686; AAP37183.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 219 AA; 25264 MW; D8BE36ABE652FCB9 CRC64;
```

```
Query Match 78.4%; Score 971; DB 2; Length 219;
Best Local Similarity 82.6%; Pred. No. 5.4e-72;
Matches 180; Conservative 17; Mismatches 21; Indels 0; Gaps 0;
```

```
Qy 9 EKDLRKSELORNALSNLROIYYNEKAITENKESDDQFLNTLLFKGFFTGHPWYNDL 68
Db 2 EKDLHKKSELOGVADLNDLROIYYHNGKAITENKESDDQFLHTLLFNGFFTDHPWYNDL 61
Qy 69 VDLGSKDATNKKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLTBEKKVPIN 128
Db 62 VDPGSKVLADKYKGVLDLYGAYYGYCAGGTGPKTKACMYGGVTLHDNNRLTBEKKVPIN 121
Qy 129 LWDGKQTVPIDKVTSKKEVTVQELDLQARHHLHGKFGLYNSDSFGKRVQGLIVFHS 188
Db 122 LMLGKQTVPIETVKTKKNVTVQELDLQARRHHLHGKFGLYNSDVDDGKRVQGLIVFHT 181
```

```
Qy 189 SEGSTVSYDLPDAQGYPTLLRIYRDNKNTINSENHIDLYLTT 226
Db 182 STEPSVYDLPFGAQGQNSNTLLRIYRDNKNTINSENHIDLYLTS 219
```

RESULT 8

```
076LS7 PRELIMINARY; PRT; 268 AA.
ID 076LS7.
AC 076LS7;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Enterococin J.
GN Name=sej;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
```

OX NCBI_TaxID=1280;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP Omoec K., Hu D., Nakane A., Shinagawa K.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB075606; BAC97796.1; -
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 SQ SEQUENCE 268 AA; 31227 MW; 016E5346079D3E20 CRC64;

 Query Match 67.6%; Score 837; DB 2; Length 268;
 Best Local Similarity 65.4%; Pred. No. 7.6e-61;
 Matches 151; Conservative 38; Mismatches 42; Indels 0; Gaps 0;

 QY 3 KEEETNEKDLRKSELSQRNALSNLRQIYYNEKAITENKESDDQPLENTLTKGPFTHGP 62
 DB 27 KNETTEKRLHKKSELSSTLNNLRHLYFENKGISSEKMTDQPLDYTLTKSPFISHS 86
 QY 63 WYNDDLVDGSKDATTNKYKGVLDYGAAYGYOCAGGTPTNKACMGVTLHDNNRLTSE 122
 DB 87 QYNDDLVDGSKETATNKFKQKQVDLYGSGGSGGKPKTKACMGVTLHNNQDLYDT 146
 QY 123 KKVPIMLWDGKQTVPIDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQK 182
 DB 147 KKVPIMLWDSIRTVPLDIVTKNNKKVTVIGELDLQARYYLLHQVLYNPSTFGKIQKG 206
 QY 183 LIVFHSSEGSTVSYDLFDAGQGYPTDLRIYRNKNTINSNHLIDLYTTT 233
 DB 207 LIVFHTSKPELVSYDLFNVIGQYPDKLKTYODNKIIESENHIDLYLTS 257

 RESULT 9
 ID 085217 PRELIMINARY; PRT; 268 AA.
 AC 085217;
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Enterotoxin J.
 GN Name=sej;
 OS Staphylococcus aureus.
 OG Plasmid p18485.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP STRAIN=KS11410;
 RX MEDLINE=99052098; PubMed=9835033;
 RA Zhang S., Iandolo J.J., Stewart G.C.;
 RT "The enterotoxin D plasmid of Staphylococcus aureus encodes a second
 RT enterotoxin determinant (sej).";
 RL FEMS Microbiol. Lett. 168:227-233(1998).
 DR EMBL; AF053140; AAC78590.1; -
 DR HSSP; P1363; IESP.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.

DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 KW Plasmid.
 SQ SEQUENCE 268 AA; 31230 MW; ACSF3546060ACE22 CRC64;

 Query Match 67.0%; Score 830; DB 2; Length 268;
 Best Local Similarity 64.9%; Pred. No. 2.9e-60;
 Matches 150; Conservative 38; Mismatches 43; Indels 0; Gaps 0;

 QY 3 KEEETNEKDLRKSELSQRNALSNLRQIYYNEKAITENKESDDQPLENTLTKGPFTHGP 62
 DB 27 KNETTEKRLHKKSELSSTLNNLRHLYFENKGISSEKMTDQPLDYTLTKSPFISHS 86
 QY 63 WYNDDLVDGSKDATTNKYKGVLDYGAAYGYOCAGGTPTNKACMGVTLHDNNRLTSE 122
 DB 87 QYNDDLVDGSKETATNKFKQKQVDLYGSGGSGGKPKTKACMGVTLHNNQDLYDT 146
 QY 123 KKVPIMLWDGKQTVPIDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQK 182
 DB 147 KKVPIMLWDSIRTVPLDIVTKNNKKVTVIGELDLQARYYLLHQVLYNPSTFGKIQKG 206
 QY 183 LIVFHSSEGSTVSYDLFDAGQGYPTDLRIYRNKNTINSNHLIDLYTTT 233
 DB 207 LIVFHTSKPELVSYDLFNVIGQYPDKLKTYODNKIIESENHIDLYLTS 257

 RESULT 10
 ID 06R2G0 PRELIMINARY; PRT; 154 AA.
 AC 06R2G0;
 DT 05-JUL-2004 (TEMBLrel. 27, Created)
 DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
 DE Enterotoxin B (Fragment).
 OS Staphylococcus aureus subsp. aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=46170;
 RN [1]
 RA SEQUENCE FROM N.A.
 RP STRAIN=ATCC 27664;
 RX PubMed=15131181;
 RA Sergeev N., Volokhov D., Chizhikov V., Raabooly A.;
 RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
 RT an oligonucleotide microarray assay.";
 RL J. Clin. Microbiol. 42:2134-2143(2004).
 DR EMBL; AY518387; AAR9635.1; -
 DR HSSP; P13380; IAN8.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strp_toxin; 1.
 DR Pfam; PF02876; Staph_Strp_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 FT NON_TER 1
 FT NON_TER 154
 SQ SEQUENCE 154 AA; 17390 MW; 10D3329E23F0C74F CRC64;

 Query Match 66.6%; Score 825; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 3.8e-60;
 Matches 154; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 QY 76 ATNKYKGVLDYGAAYGYOCAGGTPTNKACMGVTLHDNNRLTEKKVPIMLWDGKQ 135
 DB 1 ATNKYKGVLDYGAAYGYOCAGGTPTNKACMGVTLHDNNRLTEKKVPIMLWDGKQ 60
 QY 136 TVYPIDKVTSSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHSSEGSTVS 195

```
Db 61 TTVPIDKRTSKREVTYVELDQARHYLHGKFGLYNSDSFGKVGRLVPHSSGSTVS 120
QY 196 YDLFDAQGYPTTLRIYRDNKTINSENHIDLY 229
Db 121 YDLFDAQGYPTTLRIYRDNKTINSENHIDLY 154

RESULT 11
ETXD STAU STANDARD: PRT: 258 AA.
ID _ETXD STAU STANDARD: PRT: 258 AA.
AC P20723;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Enterotoxin type D precursor (SED).
GN Name:etd;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89359112; PubMed=2549000;
RA Bayles K.W., Iandolo J.J.;
RT "Genetic and molecular analyses of the gene encoding staphylococcal enterotoxin D."
RL J. Bacteriol. 171:4799-4806(1989).
RN [2]
RP SEQUENCE FROM N.A., AND X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
RX STRAIN=ATCC 23233;
RA MEDLINE=97157473; PubMed=9003758;
RA Sundstroem M., Abrahmsen L., Antonsson P., Mehindate K., Mourad W., Dohlsten M.;
RT "The crystal structure of staphylococcal enterotoxin type D reveals Zn2+-mediated homodimerization."
RL EMBO J. 15:6832-6840(1996).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
CC -1- SUBUNIT: Homodimer; zinc-dependent.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M28521; AAB06195.1; -.
DR PIR; A33953; A33953.
DR HSSP; P13163; ISXT.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_toxin_C1.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Enterotoxin; Signal; Superantigen; Toxin; Zinc.
KM SIGNAL 1
FT CHAIN 26 258 Enterotoxin type D.
FT METAL 212 212 Zinc.
FT METAL 250 250 Zinc.
FT METAL 252 252 Zinc.
FT VARIANT 114 114 P -> A (in strain ATCC 23235).
```

```
SQ SEQUENCE 258 AA; 29746 MW; 4F7C6A28D42597FD CRC64;
Query Match 53.6%; Score 663; DB 1; Length 258;
Best Local Similarity 54.5%; Pred. No. 1.6e-46;
Matches 126; Conservative 35; Mismatches 70; Indels 0; Gaps 0;
QY 1 SEKSEINEKDLRKSEIQRNALSNLRQIYYNEKAITENKESDDQFLENTLLPFGFTG 60
Db 26 NENIDSVXKEKELHKKSEISTALNNMKISYADKPIIGENKSTGQFLENTLLYKKFPTD 85
QY 61 HPWYNDLVLDGSKDATNKYKGGKVDLYGAYYGQACGTGPNKTAQWGVTLHDNNRLT 120
Db 86 LIPEDDLINNSKEMAHFYSKAVDYPPIYSINCYGSELDRRTACTGCTPHBGNLTK 145
QY 121 EEKVPINLWIDGKQTTVPIDKRTSKREVTYVELDQARHYLHGKFGLYNSDSFGKVG 180
Db 146 ERKKIPINLWINGVQKEVSLDKVQTDKKKNTVQVELDQARRYLQNDLKYNNDTLGKIQ 205
QY 181 RGLVPHSSGSTVSYDLFDAQGYPTTLRIYRDNKTINSENHIDLY 231
Db 206 RGLIEFSSDSKVSYDLFDVKGDFPEKQRLIYSDNKTLSHHLHIDLY 256

RESULT 12
ID Q6R2F9 PRELIMINARY; PRT: 152 AA.
AC Q6R2F9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin D (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=ATCC 10656;
RA Sergeev N., Volokhov D., Chizhikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by an oligonucleotide microarray assay."
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518388; AAB99636.1; -.
DR HSSP; P13380; IAN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_toxin_C1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 152
SQ SEQUENCE 152 AA; 17514 MW; F0354318924CB739 CRC64;
Query Match 40.1%; Score 496; DB 2; Length 152;
Best Local Similarity 59.9%; Pred. No. 4.8e-33;
Matches 91; Conservative 22; Mismatches 39; Indels 0; Gaps 0;
QY 80 YGKKVNDLYGAYYGQACGTGPNKTAQWGVTLHDNNRLTEKKVPINLWIDGKQTTVP 139
Db 1 FKSKNVDYAIRYSINCYGSELDRRTACTGCTPHBGNLTKERKKIPINLWINGVQKEVS 60
QY 140 IDKRTSKREVTYVELDQARHYLHGKFGLYNSDSFGKVGRLVPHSSGSTVSYDLF 199
Db 61 LDKVQTDKKKNTVQVELDQARRYLQNDLKYNNDTLGKIQRKIEFSSDSKVSYDLF 120
QY 200 DAQGYPTTLRIYRDNKTINSENHIDLY 231
```


Db 121 DYKGFPEKQRLRYSDNKTSLSTREHMLHIDLYL 152

RESULT 13

Q8NM97 PRELIMINARY; PRT; 229 AA.

AC Q8NM97; 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE MM1552 protein.
 GN OrderedLocuNames=MM1552;
 OS Staphylococcus aureus (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=156620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12043378; DOI=10.1016/S0140-6736(02)08713-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RA "Genome and virulence determinants of high virulence community-
 RT acquired MRSA";
 RL Lancet 359:1819-1827(2002).
 DR EMBL; AP004827; BAB5417.1; -.
 DR HSP; P13163; ISXT.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strept_tox.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 KW SEQUENCE 229 AA; 26728 MW; AD3DAF9EALAE3677 CRC64;

Query Match 39.6%; Score 490.5; DB 2; Length 229;
 Best Local Similarity 39.4%; Pred. No. 2.2e-32;
 Matches 91; Conservative 48; Mismatches 87; Indels 5; Gaps 3;

QY 1 SEKSEIN EKDKRKSELQNALSNLRQIYYNEKAITENKESDDPLENTLLFKGFPTG 60
 Db 2 TNSASAI EYSDLHNHKSFKPSKRLSNK-MSFINPTQL-EKNTNDLKHDDLPHDMFTN 59
 QY 61 HPWYNDLVLDGSKDANTKYGKVDLYGAYGYOCAGTPTNKATACMYGGVTLHNNRLT 120
 Db 60 DMKKDKFKYEFENALSKFKINDIDIFAGNYGGCGATNTQCSYGVTLSDNNKYD 119
 QY 121 EEKKVPINIMDGKQTTVPIDKYTSKKEVTVQELDLQARHYLHGKGLYNSPSFGKVQ 180
 Db 120 DYKNIPCNIMIDGQAEIELTAVTKTKKIYTIQELDVQLRNYINERKYLQE--GGDIY 176
 QY 181 RGLIVHSESGTSVSYDLDPDAGQYPTLLIRYRDKNTINSEMLHIDLYL 231
 Db 177 KGVYKYNHNDDEONIEYFNINLGEYGVYEVALKMTADNKTINSKDLHDIYLF 227

RESULT 14

Q6G8W7 PRELIMINARY; PRT; 229 AA.

AC Q6G8W7; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Putative enterococin.
 GN OrderedLocuNames=SA51538;

OS Staphylococcus aureus (strain MSSA476).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=282459;
 RN [1]

RP SEQUENCE FROM N.A.
 RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
 RA Holden M.T.G., Fell B.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
 RA Bason N.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
 RA Bason N., Bentley S.D., Chillingworth T., Chillingworth T.,
 RA Churcher C., Clark L., Corton C., Cronin A., Doggett J., Dowd L.,
 RA Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
 RA James K.D., Leonard N., Line A., Mayes R., Moutle S., Mungall K.,
 RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
 RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
 RA Spratt B.G., Parkhill J.;
 RT "Complete genomes of two clinical Staphylococcus aureus strains:
 RT evidence for the rapid evolution of virulence and drug resistance."
 RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
 DR EMBL; BX571857; CAG4333.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strept_tox.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_Strep_toxin; 1.
 DR Pfam; PF02876; Staph_Strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 KW SEQUENCE 229 AA; 26728 MW; AD3DAF9EALAE3677 CRC64;

Query Match 39.6%; Score 490.5; DB 2; Length 229;
 Best Local Similarity 39.4%; Pred. No. 2.2e-32;
 Matches 91; Conservative 48; Mismatches 87; Indels 5; Gaps 3;

QY 1 SEKSEIN EKDKRKSELQNALSNLRQIYYNEKAITENKESDDPLENTLLFKGFPTG 60
 Db 2 TNSASAI EYSDLHNHKSFKPSKRLSNK-MSFINPTQL-EKNTNDLKHDDLPHDMFTN 59
 QY 61 HPWYNDLVLDGSKDANTKYGKVDLYGAYGYOCAGTPTNKATACMYGGVTLHNNRLT 120
 Db 60 DMKKDKFKYEFENALSKFKINDIDIFAGNYGGCGATNTQCSYGVTLSDNNKYD 119
 QY 121 EEKKVPINIMDGKQTTVPIDKYTSKKEVTVQELDLQARHYLHGKGLYNSPSFGKVQ 180
 Db 120 DYKNIPCNIMIDGQAEIELTAVTKTKKIYTIQELDVQLRNYINERKYLQE--GGDIY 176
 QY 181 RGLIVHSESGTSVSYDLDPDAGQYPTLLIRYRDKNTINSEMLHIDLYL 231
 Db 177 KGVYKYNHNDDEONIEYFNINLGEYGVYEVALKMTADNKTINSKDLHDIYLF 227

RESULT 15

Q7A2O6 PRELIMINARY; PRT; 258 AA.

AC Q7A2O6; 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Enterococin.
 GN Name=sen; OrderedLocuNames=SAV1825;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN [1]

RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
 RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003363; BAB57987.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactr_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR Pfam: PF02876; Staph_stp_tox_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

QY EINEKDLAKKSELQNALSNLRQIYYNKAIT-----ENKESDQPLENTLLPFKFFTG 60
DB 32 EVDKDLKKKSDLBSSKLFNLTLS--YYTD--ITWQDLSNKISTDQLNNTIILKNIDIS 87
QY 61 HPWYNDLLVDLGSXDATNRYKAKVDLYGAYGYQACAGTPNKTAQMTGGVTLHDNNRLT 120
DB 88 VLKTSLSLKVEFNSSDLANQFGKNIDYGLYFGNKCVCGLTEKTSCLYGVTHDGNQDLD 147
QY 121 EEKVPINLMDGKQTTPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
DB 148 EEKYGAVVAFDQVQEGFV--IKTKKAKVTVOELDTVRFLNLYKIYKNDT--GNIQ 203
QY 181 RGLIVFHS--SEGTSVSYDLFDQAGQVPTLLRLIYRDNKNTINSENLHIDLVL 231
DB 204 KGCIFFSHNNQDQSFYIDLNVKGSVGAEPFQYSDNRVTSSSNYHIDVFLY 256

RESULT 16
Q7A4X1 PRELIMINARY; PRT; 258 AA.
AC Q7A4X1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin Sen.
GN Name=sen; OrderedLocustNames=SA1643;
OS *Staphylococcus aureus* (strain N315).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=158879;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama T., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kanamori M., Matsumaru H., Matuyama A., Murakami H., Hoshiyama A.,
RA Mitutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaio C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
RT "Whole genome sequencing of methicillin-resistant *Staphylococcus*
RT aureus."
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003363; BAB42911.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.

DR InterPro: IPR006177; Bactr_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR Pfam: PF02876; Staph_stp_tox_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;
Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

QY EINEKDLAKKSELQNALSNLRQIYYNKAIT-----ENKESDQPLENTLLPFKFFTG 60
DB 32 EVDKDLKKKSDLBSSKLFNLTLS--YYTD--ITWQDLSNKISTDQLNNTIILKNIDIS 87
QY 61 HPWYNDLLVDLGSXDATNRYKAKVDLYGAYGYQACAGTPNKTAQMTGGVTLHDNNRLT 120
DB 88 VLKTSLSLKVEFNSSDLANQFGKNIDYGLYFGNKCVCGLTEKTSCLYGVTHDGNQDLD 147
QY 121 EEKVPINLMDGKQTTPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGKQV 180
DB 148 EEKYGAVVAFDQVQEGFV--IKTKKAKVTVOELDTVRFLNLYKIYKNDT--GNIQ 203
QY 181 RGLIVFHS--SEGTSVSYDLFDQAGQVPTLLRLIYRDNKNTINSENLHIDLVL 231
DB 204 KGCIFFSHNNQDQSFYIDLNVKGSVGAEPFQYSDNRVTSSSNYHIDVFLY 256

RESULT 17
Q9EZM4 PRELIMINARY; PRT; 258 AA.
AC Q9EZM4;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SEN.
GN Name=sen;
OS *Staphylococcus aureus*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarrard S., Peyrat M.A., Lim A., Tristram A., Bes M., Mougel C.,
RA Etienne J., Vandenesch F., Bonneville M., Lina G.,
RT "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superantigens in *Staphylococcus aureus*."
RL J. Immunol. 166:669-677(2001).
DR EMBL: AF285760; AAG36956.1; -
DR PIR: H89968; H89968.
DR HSSP: Q53585; 1P77.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactr_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_stp_toxin_1.
DR Pfam: PF02876; Staph_stp_tox_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29676 MW; 8A6C074F3E1F82D2 CRC64;

Query Match 37.3%; Score 461.5; DB 2; Length 258;
Best Local Similarity 41.2%; Pred. No. 6.4e-30;

Matches 96; Conservative 45; Mismatches 77; Indels 15; Gaps 6;

```

QY 6 EINEKDLRKSELRNALSNLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
DB 32 EVDKDLKKKSDLSKSLFNLTSS--YYTD--ITWQDSESNKISTDQLANNITILKXIDIS 87
QY 61 HPWYNLDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTPTNKTCAMYGAVTLHDNNRLT 120
DB 88 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVITLYDGNQDLD 147
QY 121 EEKVPINIMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDFSGKQVQ 180
DB 148 EEKVGIVNVPKQGVQDEGFV--IKTKKAKVTVQELDTKVRFKLEMLYKIKYNKDT--GNIQ 203
QY 181 RGLIVFHS--SGSTVSYDLFDAQGYPTTLRIYRDNKTINSENHIDLXYL 231
DB 204 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDNTVSSNHYHIDVFLY 256

```

RESULT 18

```

ID 06G6CN3 PRELIMINARY; PRT; 251 AA.
AC 06G6CN3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin SEB variant.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=382;
RA MEDLINE=2692404; PubMed=12807452;
RA Letertre C., Perelle S., Dilaeser F., Pach P.;
RT "Identification of a new putative enterotoxin SEB encoded by the egc
RT cluster of Staphylococcus aureus.";
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL: AY158703; ANO17733.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBFB6BA40 CRC64;

```

Query Match 36.1%; Score 446.5; DB 2; Length 251;
 Best Local Similarity 39.5%; Pred. No. 1.1e-28;
 Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

```

QY 6 EINEKDLRKSELRNALSNLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
DB 25 DVDKDLKKKSDLSKSLFNLTSS--YYTD--ITWQDSESNKISTDQLANNITILKXIDIS 80
QY 61 HPWYNLDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTPTNKTCAMYGAVTLHDNNRLT 120
DB 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVITLYDGNQDLD 140
QY 121 EEKVPINIMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDFSGKQVQ 180
DB 141 EEKVGIVNVPKQGVQDEGFV--IKTKKAKVTVQELDTKVRFKLEMLYKIKYNKDT--GNIQ 196
QY 181 RGLIVFHS--SGSTVSYDLFDAQGYPTTLRIYRDNKTINSENHIDLXYL 231
DB 197 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDNTVSSNHYHIDVFLY 249

```

RESULT 19

```

ID 06G6FN1 PRELIMINARY; PRT; 251 AA.
AC 06G6FN1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN Ordered locus names=SA1917;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=282458;
RN (1)
RP SEQUENCE FROM N.A.
RC PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Baason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulie S., Mungall K.,
RA Ormond D., Quail M.A., Rabinovitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40903.1;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 251 AA; 28806 MW; 1E2966FBFB6BA40 CRC64;

```

Query Match 36.1%; Score 446.5; DB 2; Length 251;
 Best Local Similarity 39.5%; Pred. No. 1.1e-28;
 Matches 92; Conservative 49; Mismatches 77; Indels 15; Gaps 6;

```

QY 6 EINEKDLRKSELRNALSNLRQIYYNEKAIT-----ENKESDDQPLENTLLFKGFFTG 60
DB 25 DVDKDLKKKSDLSKSLFNLTSS--YYTD--ITWQDSESNKISTDQLANNITILKXIDIS 80
QY 61 HPWYNLDLVDLGSKDATNKYKGGKVDLYGAYYGOCAGTPTNKTCAMYGAVTLHDNNRLT 120
DB 81 VLKTSLSKVEFNSSDLANQFKGNIDYGLYGNKCVGLTEKTSCLYGGVITLYDGNQDLD 140
QY 121 EEKVPINIMIDGKQTTVPIDKVTSSKEVTVQELDLQARHYLHGKFGLYNSDFSGKQVQ 180
DB 141 EEKVGIVNVPKQGVQDEGFV--IKTKKAKVTVQELDTKVRFKLEMLYKIKYNKDT--GNIQ 196
QY 181 RGLIVFHS--SGSTVSYDLFDAQGYPTTLRIYRDNKTINSENHIDLXYL 231
DB 197 KGCIFPHSHNHQDSFYDLYNVKGSVGAEPFQFYSNDNTVSSNHYHIDVFLY 249

```

```
GN OrderedLocustNames=SAR1921;
OS Staphylococcus aureus (strain MRS252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCB1_TaxID=282458;
[1]
RP SEQUENCE FROM N.A.
RA PubMed:15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barton A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagsels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Partridge J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL; BX571856; CAG40907.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph_Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 254 AA; 29447 MW; E2ECD141E300CD9 CRC64;

Query Match 33.4%; Score 414; DB 2; Length 254;
Best Local Similarity 40.9%; Pred. No. 5,1e-26;
Matches 99; Conservative 39; Mismatches 84; Indels 20; Gaps 7;

QY 1 SEKSEINEKDLRKSEIQRNALSNLRQIYYNEKATENKE--SDQFLENTLTFKGF 59
DB 23 NEENPKT--EDLCKSSVDYDLAHNIDKDYMNRTNESYTLTEKELDLDLRFNF-- 78
QY 60 GHPW-----YNDLVLVDSKDATNKYKGGKVDLYGAYYGQACGTPNKTACMYGV 112
DB 79 --TWLDGSAEPKDLKVEFSSSEISKEYFGKVDYIGVYKAKHGCHGVQVKTACTYGGV 136
QY 113 LHDNNRLTEKKVPIINLMIDGKQTVPIIDKVTISKETVTVQELDQARHYLHGKFGLYN 172
DB 137 PHENNKLSPEKPIGVAAYKDNVNVNFTI--VTTDKKVTQAEOLDIKVTKLNNAVYKLY-- 192
QY 173 DSFGGKVGRLIVFHSSEGSTVS--YDLFDAQGYPTLLRIYRDNKTINSENLHIDL 230
DB 193 DRMTSDVQKGYIKFHSSEHKSFFYDLYFKGNLPDQYLQIYNDNKTIDSVDYHIDV 252
QY 231 YT 232
DB 253 FT 254

RESULT 21
Q99746 PRELIMINARY; PRT; 260 AA.
AC Q99746;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin.
GN Name=seo; OrderedLocustNames=SAV1830; ATCC 700699).
OS Staphylococcus aureus (strain MRS252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCB1_TaxID=158878;
[1]
```

```
RP SEQUENCE FROM N.A.
RC STRAIN=M50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiratake K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
RL EMBL; AP003363; BAB57992.1; -.
DR PIR; E89969; E89969.
DR HSSP; Q54971; 1BXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 260 AA; 29836 MW; AC927DDCC3E3B8EF CRC64;

Query Match 31.3%; Score 387.5; DB 2; Length 260;
Best Local Similarity 39.9%; Pred. No. 8e-24;
Matches 97; Conservative 31; Mismatches 86; Indels 29; Gaps 8;

QY 8 NEKD-----LKKSELRNALSNLRQIYYNE----FATENKSSDQFLENTLTFKGF 58
DB 29 NEEDPKIESLCKSSVDPDLAHNIDNDINNRTFTVSVISTTE--KFLPDFLLFSI- 84
QY 59 TGHFW-----YNDLVLVDSKDATNKYKGGKVDLYGAYYGQACGTPNKTACMYGV 111
DB 85 ---NWLDSIAEPKDLKVEFSSSAISKEFLKQVYIGVYKAKHGCHGVQVKTACTYGGV 141
QY 112 TLHDNNRLTEKKVPIINLMIDGKQTVPIIDKVTISKETVTVQELDQARHYLHGKFGLYN 171
DB 142 TPHENNKLSPEKPIGVAAYKDNVNVNFTI--VTTDKKVTQAEOLDIKVTKLNNAVYKLY- 198
QY 172 SDSFGKVGRLIVFHSSEGSTVS--YDLFDAQGYPTLLRIYRDNKTINSENLHIDL 229
DB 199 -DRMTSDVQKGYIKFHSSEHKSFFYDLYFKGNLPDQYLQIYNDNKTIDSVDYHIDV 257
QY 230 LYT 232
DB 258 LFT 260

RESULT 22
Q7A4W6 PRELIMINARY; PRT; 260 AA.
AC Q7A4W6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin Seo.
GN Name=seo; OrderedLocustNames=SA1648;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCB1_TaxID=158879;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-O., Ito T.,
```



```

Best Local Similarity 48.7%; Pred. No. 1.8e-23;
Matches 73; Conservative 24; Mismatches 53; Indels 0; Gaps 0;

QY 1 SEKSEINEKDLRKSELSORNALSNLRQIYYNEKAITENKESDQFLENTLLFKGFPTG 60
Db 26 NENIDSVKELHKSELSSTRLNMMKSYADKNIIGENKSTGQFLENTLLFKGFPTD 85
QY 61 HPWYNDLLVDGSKDATNRKYGKVDLYGAYYGACGTPNKTCMYGGVTLHDNNRLT 120
Db 86 LINFEDLLINFNSKEMAGHFKSKNDVYPIRYSINCYGEIDTACTYGGVTPHEGNLTK 145
QY 121 EEKVPIPLNLDGKQTYPIDKVTSKEV 150
Db 146 ERKKIPIPLNMGVQEVSLDKVQTDKNL 175

RESULT 25
Q8RR76 PRELIMINARY; PRT; 217 AA.
AC Q8RR76;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin H (Fragment).
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21871379; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shinagawa K.;
RT "Detection of seh, seh, and seh genes in Staphylococcus aureus
RT isolates and determination of the enterotoxin productivities of S.
RT aureus isolates Harboring seh, seh, or seh genes.";
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060536; BAB85990.1; -.
DR HSSP; Q53585; IEWC.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph_toxin.
DR Pfam; PF01123; Staph_toxin_1.
DR Pfam; PF02876; Staph_toxin_C_1.
DR PRINTS; PR00279; BACTRTOXIN_
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 217 AA; 25143 MW; ABA44E23F31DE80D CRC64;

Query Match 29.6%; Score 366; DB 2; Length 217;
Best Local Similarity 37.9%; Pred. No. 3.8e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;

QY 10 KDLRKSELSORNALSNLRQIYYNEKAITENKESDQFLENTLLFKGFPTGHPWYNDLLV 69
Db 1 EDLHDKSELDTLALAN--AYGQYNHPFIKENIKSDIEGKOLIFRN--QGDSG--NDLRV 55
QY 70 DLGSDAIDNKKYKGVLDYGAAYYGACGTPNKTCMYGGVTLHDNNRLTBEKKVPNTL 129
Db 56 KFAADLAQKFKKNKVDIYGASFFYKCKEISENISECYGGTTL--NSEKLAQERYIGANV 114
QY 130 WIDGQTFVPIDKVTSKEVTVQELDLQARHYLHGKGLYNSDFGKVGORGLIVPSS 189
Db 115 WVDGIQKTEL--IRTNKANTLQELDIKIKILSDKIKIYKDS---EISGLIEFDMK 169
QY 190 EGSFVSYDLFDAGGQYPTLLRIYRDNKTINSENL-HIDLVLTYT 232
Db 170 TPRDYSFDIYDLKGENDYEIDKTYEDNKTLSKSDISHIDVNLTYT 213

RESULT 26

```

```

ETXH STAHM
ID ETXH STAHM STANDARD; PRT; 241 AA.
AC Q53585;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Enterotoxin type H precursor (SEH).
GN Name=entH; Synonyms=seh; Ordered locus names=MM0051;
OS Staphylococcus aureus (strain MW2), and
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620, 1280;
RN [1]
RP SEQUENCE FROM N.A., PARTIAL SEQUENCE, AND CHARACTERIZATION.
RC STRAIN=D4508;
RX MEDLINE=95053699; PubMed=7964453;
RA Ren K., Bannan J.D., Pancholi V., Cheung A.L., Robbins J.C.,
RA Fieschetti V.A., Zabriekie J.B.;
RT "Characterization and biological properties of a new staphylococcal
RT exotoxin.";
RL J. Exp. Med. 180:1675-1683(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yamamoto K., Hiramatsu K.;
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA.";
RL Lancet 359:1819-1827(2002).
RN [3]
RP X-RAY CRYSTALLOGRAPHY (1.69 ANGSTROMS).
RX PubMed=10986116; DOI=10.1006/jmbi.2000.4093;
RA Hakansson M., Petersson K., Nilsson H., Forsberg G., Bjoerk P.,
RA Antonsson P., Svensson L.A.;
RT "The crystal structure of staphylococcal enterotoxin H: implications
RT for binding properties to MHC class II and TCR molecules.";
RL J. Mol. Biol. 302:527-537(2000).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- COPACOR: Binds 1 zinc ion per subunit. The zinc ion is necessary
CC for the toxin interaction with MHC class II.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/announcements
CC or send an email to license@ebi.ac.uk).
CC -----
DR EMBL; U11702; AAA19777.1; -.
DR EMBL; AP004822; BAB93916.1; -.
DR PDB; 1ENF; X-ray; A=26-237.
DR PDB; 1EWC; X-ray; A=26-239.
DR PDB; 1F77; X-ray; A/B=25-241.
DR PDB; 1HXV; X-ray; D=25-237.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph_toxin.
DR InterPro; IPR006126; Staph_toxin.
DR InterPro; IPR006173; Staph_toxin.
DR Pfam; PF02876; Staph_toxin_C_1.
DR Pfam; PF01123; Staph_toxin_1.
DR PRINTS; PR00279; BACTRTOXIN_
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; FALSE_NEG.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

```

3D-structure: Complete proteome; Direct protein sequencing;
KM Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
FT SIGNAL 1 24 Enterotoxin type H.
FT CHAIN 25 241
FT METAL 230 230 Zinc.
FT METAL 232 232 Zinc.
FT DISULFID 106 116
SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;
Query Match 29.6%; Score 366; DB 1; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKSDQPLENTLLFPKGFTHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLKV 79
QY 70 DLGSKDATNKKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEBKVPINL 129
DB 80 KRATADLAQKFNKQNDVIGASFYKCEKISENISECLVGGTLL-NSEKLAQGRVIGANV 138
QY 130 WIDGKQTVPIIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKQVTLQELDIKIRKILSDKVIKYKDS--EISKGLIEFDK 193
QY 190 EGSSTVSYDLFDAQGYPTLLRIYRDNKTINSENT-HIDLXYT 232
DB 194 TRDYSFDIYDLKGENDYEDIKIYEDNKTLSKSDISHIDVNLV 237
RESULT 27
QYVAM8 PRELIMINARY; PRT; 241 AA.
ID 06VAM8; 06VAM8;
AC 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin H precursor.
GN Name=seh;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN 11
RP SEQUENCE FROM N.A.
RC STRAIN=FRI 137;
RA Gul'ko L.B., Voyushin K.E., Fluer F.S., Okorokova N.A., Krivenko M.S.,
Vei'ko V.P., Debabov V.G.;
RT "The Obtaining of the Tumor-Addressed Genetically Engineered Drug for
RT Cancer Immunotherapy. II. Cloning a Gene of the pro-Enterotoxin H (seh)
RT from Staphylococcus aureus, Its Expression in *Bacterichia coli*.
RT Investigation of the Enterotoxin H Secretion by *E. coli* Cells.";
RL Biotechnology 6:172-78(2003).
DR EMBL: AY45144; AA063188.1; -;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal.
FT SIGNAL 1 24 Enterotoxin H.
FT CHAIN 25 241
SQ SEQUENCE 241 AA; 27831 MW; 70EBB8418C9CC6E CRC64;
Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKSDQPLENTLLFPKGFTHPWYNDLLV 69

DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLKV 79
QY 70 DLGSKDATNKKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEBKVPINL 129
DB 80 KRATADLAQKFNKQNDVIGASFYKCEKISENISECLVGGTLL-NSEKLAQGRVIGANV 138
QY 130 WIDGKQTVPIIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKQVTLQELDIKIRKILSDKVIKYKDS--EISKGLIEFDK 193
QY 190 EGSSTVSYDLFDAQGYPTLLRIYRDNKTINSENT-HIDLXYT 232
DB 194 TRDYSFDIYDLKGENDYEDIKIYEDNKTLSKSDISHIDVNLV 237
RESULT 28
QYVAM8 PRELIMINARY; PRT; 241 AA.
ID 06GD45; 06GD45;
AC 06GD45; 06GD45;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin H.
GN Name=seh; OrderedlocusNames=SAS0051;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=282459;
RN 11
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
Bason N., Bentley S.D., Chillingworth C., Chillingworth T., Dowd L.,
Churcher C., Clark L., Cotton A., Cronin A., Doggett J., Dowd L.,
Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
Ormond D., Quail M.A., Rabinowitch B., Rutherford K.M., Sanders M.,
Sharp S., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
RL EMBL: BX571857; CAG41819.1; -;
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:patogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_toxin; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW complete proteome.
SQ SEQUENCE 241 AA; 27858 MW; 70F77985877616CE CRC64;
Query Match 29.6%; Score 366; DB 2; Length 241;
Best Local Similarity 37.9%; Pred. No. 4.3e-22;
Matches 85; Conservative 46; Mismatches 81; Indels 12; Gaps 7;
QY 10 KDLRKSELDQRLNLSNRQIYYNNEKAITENKSDQPLENTLLFPKGFTHPWYNDLLV 69
DB 25 EDLHDKSELTDLALAN--AYGQYNHPFIKENIKSDISEGKDLIFRN--QGDSG-NDLKV 79
QY 70 DLGSKDATNKKYKGVKVDLYGAYVYQACAGTPNKTCAMYGVTLLHDNNRLTEBKVPINL 129
DB 80 KRATADLAQKFNKQNDVIGASFYKCEKISENISECLVGGTLL-NSEKLAQGRVIGANV 138
QY 130 WIDGKQTVPIIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFGKVGQGLIVFHS 189
DB 139 WVDGIQKETEL--IRTNKKQVTLQELDIKIRKILSDKVIKYKDS--EISKGLIEFDK 193

```
Qy 190 EGSIVSYDLFPAQGYPTTLRLIRYDNKTINSNT-HIDLVIYT 232
Db 194 TPRDYSFDIYDLKGENDYEIDKIYEDNKTLSKSDISHIDVNLXT 237

RESULT 29
Q6YCN5 PRELIMINARY; PRT; 242 AA.
ID Q6YCN5;
AC Q6YCN5;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Enterotoxin SEI variant.
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
RX NCBI_TaxID=1280;
RP [1]
SEQUENCE FROM N.A.
RC STRAIN=382F;
RA MEDLINE=22692404; PubMed=12807452;
RA Leterre C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin SEU encoded by the egc
cluster of Staphylococcus aureus.";
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY158703; AA01731.1; -.
DR HSSP; P13380; 1AN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STRAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;

Query Match 28.2%; Score 348.5; DB 2; Length 242;
Best Local Similarity 36.6%; Pred. No. 1.2e-20;
Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;

Qy 8 NEKDIRKSELRN-ALSNLRQIY---YNEKAITENKESDDQPLENTLLFKGFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRFYTKYDIIDLKGYTDKLPANQLE-----FSTG-- 64
Qy 63 WYNLDLVDSKDATNKYKGGKVDLYGAVYGCAGGTPNKTACMYGVTLDHNNRLTEE 122
Db 65 -TNDLISESNWDEISRKFGKMDIFGIDYNGPC-----KTKMYGGATL-SCGYLNSA 116
Qy 123 KVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK-- 178
Db 117 RKIPINLWINGKHKTISTDKATINKKLVTAQEDIVKARLYOEENIYGHNNNGKXGYG 176
Qy 179 -----VQGLIVFHSSEGSTVSYDLFPAQGYPTTLRLIRYDNKTINSNT-HIDL 228
Db 177 YKSKFYSGFNKGKVLFLHNDEKSFSDYDLFYTGDLGVFSLKIYEDNKTIISEKFLHDV 234

RESULT 30
Q6GFM9 PRELIMINARY; PRT; 242 AA.
ID Q6GFM9;
AC Q6GFM9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DE Enterotoxin.
OS OrderedLocustNames=SAR1919;
OC Staphylococcus aureus (strain MRSa252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
RX NCBI_TaxID=282458;
RP [1]
SEQUENCE FROM N.A.
```

```
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Houghton M.T.G., Feil E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Bason N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Felwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagers K.,
RA James K.D., Lennard N., Line A., Mayes R., Moulé S., Mungall K.,
RA Ormond D., Quail M.A., Rabinowitsch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Barrell B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40905.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_C; 1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN_
DR PROSITE; PS00278; STRAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 27950 MW; 5935658E21C4C89C CRC64;

Query Match 28.2%; Score 348.5; DB 2; Length 242;
Best Local Similarity 36.6%; Pred. No. 1.2e-20;
Matches 87; Conservative 37; Mismatches 77; Indels 37; Gaps 9;

Qy 8 NEKDIRKSELRN-ALSNLRQIY---YNEKAITENKESDDQPLENTLLFKGFTGHP 62
Db 17 NIKDL---SYAQGDIGVGNLRFYTKYDIIDLKGYTDKLPANQLE-----FSTG-- 64
Qy 63 WYNLDLVDSKDATNKYKGGKVDLYGAVYGCAGGTPNKTACMYGVTLDHNNRLTEE 122
Db 65 -TNDLISESNWDEISRKFGKMDIFGIDYNGPC-----KTKMYGGATL-SCGYLNSA 116
Qy 123 KVPINLWIDGKQTVPIDKVTSKKEVTVOELDLQARHYLHGKFGLYNSDSFG-GK-- 178
Db 117 RKIPINLWINGKHKTISTDKATINKKLVTAQEDIVKARLYOEENIYGHNNNGKXGYG 176
Qy 179 -----VQGLIVFHSSEGSTVSYDLFPAQGYPTTLRLIRYDNKTINSNT-HIDL 228
Db 177 YKSKFYSGFNKGKVLFLHNDEKSFSDYDLFYTGDLGVFSLKIYEDNKTIISEKFLHDV 234

RESULT 31
Q8VVM1 PRELIMINARY; PRT; 225 AA.
ID Q8VVM1;
AC Q8VVM1;
DT 01-MAR-2002 (TREMBlrel. 20, Created)
DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
DE Enterotoxin I.
GN Name=SpeI;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
RX NCBI_TaxID=1314;
RP [1]
SEQUENCE FROM N.A.
RC STRAIN=M1;
RA MEDLINE=21259899; PubMed=11359827;
RA Proft T., Arcus V.L., Handley V., Baker E.N., Fraser J.D.;
RT "Immunological and biochemical characterization of streptococcal
RT pyogenic exotoxins I and J (SPE-I and SPE-J) from Streptococcus
RT pyogenes.";
RL J. Immunol. 166:6711-6719(2001).
DR EMBL; AF438524; AAL31571.1; -.
DR HSSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
```


DR GO:0009405; P:pathogenesis; IEA.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR PROSITE; PS00279; BACTRLTOXIN.
 SQ SEQUENCE 225 AA; 25654 MW; DB19366780ACDAF CRC64;

Query Match 27.4%; Score 341.5; DB 2; Length 225;
 Best Local Similarity 34.8%; Pred. No. 4, 2e-20;
 Matches 77; Conservative 42; Mismatches 79; Indels 23; Gaps 6;

QY 25 NLRQIYYNEKAITENKESDDQPLENTLLFKGFTGHPWYN---DLLVDGSKDQATNKK 81
 DB NLRNLSTVDPEVKKKINSGPPGSLFYKNI---PYGNSIEELKVELINSYEKANPFS 63
 QY 82 GKXVDLYGAYGYQACGGTPTNKTACMYGGVTLHDNNRLTEKKVPIPLMWIDG---KQTV 138
 DB 64 GKXVDLYGAYGYQACGGTPTNKTACMYGGVTLHDNNRLTEKKVPIPLMWIDG---KQTV 119
 QY 139 PIDKVTSTKKEVTVQSELDQARHYLHGKFGLY-----NSDSFGKVGQGLIYFHS 189
 DB 120 DISTSTDKKEVTVQSELDQARHYLHGKFGLY-----NSDSFGKVGQGLIYFHS 179
 QY 190 EGSTVSYDLEFDAQGYPTLLRIYRDNKTINSENLHIDL 230
 DB 180 SGERISYTNLFDTGHGDRSMLKKYSNDKTAVSQDLHIDYL 220

RESULT 32

085383 PRELIMINARY; PRT; 242 AA.

AC 085383;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Extracellular enterotoxin type I precursor (SEI).
 GN Name=SEI; Synonym=sei;
 OS Staphylococcus aureus;
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=1280;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=FR1445;
 RX MEDLINE=98298056; PubMed=9632603;
 RA Munson S.H.; Tremaine M.T.; Betley M.J.; Welch R.A.;
 RT "Identification and characterization of staphylococcal enterotoxin
 RT types G and I from Staphylococcus aureus.";
 RL Infect. Immun. 66:337-3348(1998).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=A900322;
 RX MEDLINE=20571956; PubMed=11123352;
 RA Jarraud S.; Peyrat M.A.; Lim A.; Tristan A.; Bes M.; Mougel C.;
 RA Etienne J.; Vandenesch F.; Bonneville M.; Lina G.;
 RT "necr, a highly prevalent operon of enterotoxin gene, forms a putative
 RT nursery of superantigens in Staphylococcus aureus.";
 RL J. Immunol. 166:669-677(2001).
 DR EMBL; AF064774; AAC26661.1; -.
 DR EMBL; AF285760; AAC36953.1; -.
 DR PIR; C89969; C89969.
 DR HSSP; P13380; 1KTK.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR SIGNAL.

FT SIGNAL 1 24 Potential.
 SQ CHAIN 25 242 enterotoxin type I.
 SQ SEQUENCE 242 AA; 27863 MW; C5C8B4ACEB5414A8 CRC64;
 Query Match 27.4%; Score 339.5; DB 2; Length 242;
 Best Local Similarity 35.6%; Pred. No. 6, 7e-20;
 Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIYY---YNEKAITENKESDDQPLENTLLFKGFTGHPWYNLLVDGSKDQATN 78
 DB 30 VGNLRNFRYTKHYDIDKGYTDLPIANQLE-----PSTG---TNDLISESNMDEIS 79
 QY 79 KYXGKVDLYGAYGYQACGGTPTNKTACMYGGVTLHDNNRLTEKKVPIPLMWIDGKQTV 138
 DB 80 KFXGKLDIFGIDYDYNPPC-----KSKWYGGATL-SCGYLSARKIPINLWVGKHKTI 132
 QY 139 PIDKVTSTKKEVTVQSELDQARHYLHGKFGVNSDSFG---GK-----VQRGGLIVE 186
 DB 133 STDKIATNNKLLVQAQIDVLAERYLOEERNYIGHANNFGKKEYGYSKFYSGFNNKGVLF 192
 QY 187 HSESGSTVSYDLEFDAQGYPTLLRIYRDNKTINSENLHIDL 228
 DB 193 HANNEKSFYDLEFYTGDLGPFVSLKIYEDNKIIESKPHLDV 234

RESULT 33

07A205 PRELIMINARY; PRT; 242 AA.

AC 07A205;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Extracellular enterotoxin type I.
 GN Name=sei; OrderedlocusNames=SAV182;
 OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxID=158878;
 RN (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M.; Ohta T.; Uchiyama I.; Baba T.; Yuzawa H.; Kobayashi I.;
 RA Cui L.; Oguchi A.; Aoki K.-I.; Nagai Y.; Iian J.-Q.; Ito T.;
 RA Kanamori M.; Matsumaru H.; Maruyama A.; Murakami H.; Hoshoyama A.;
 RA Mizutani-Ui Y.; Takahashi N.K.; Sawano T.; Inoue R.-I.; Kaito C.;
 RA Sekizima K.; Hirakawa H.; Kohara S.; Goto S.; Yabuuchi J.;
 RA Kanehisa M.; Yamashita A.; Oshima K.; Furuya K.; Yoshino C.; Shiba T.;
 RA Hattori M.; Ogasawara N.; Hayashi H.; Hiratake K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus.";
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003363; BAB57990.1; -.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006173; Staph_tox_OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox_C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR COMPLETE PROTEOME.
 SQ SEQUENCE 242 AA; 27863 MW; C5C8B4ACEB5414A8 CRC64;
 Query Match 27.4%; Score 339.5; DB 2; Length 242;
 Best Local Similarity 35.6%; Pred. No. 6, 7e-20;
 Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;

QY 23 LSNLRQIYY---YNEKAITENKESDDQPLENTLLFKGFTGHPWYNLLVDGSKDQATN 78
 DB 30 VGNLRNFRYTKHYDIDKGYTDLPIANQLE-----PSTG---TNDLISESNMDEIS 79
 QY 79 KYXGKVDLYGAYGYQACGGTPTNKTACMYGGVTLHDNNRLTEKKVPIPLMWIDGKQTV 138

```
Db      80 KFKGKKLDIFGIDVNGPC-----KSKYMGATLL-SCQYLNSARKIPINLMWNKHKHTI 132
      139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQRLIVF 186
      133 STDKATNKGLVTAGQIDVKKRLRYQOEENITIGHNNTGKGEYKSKFYSFNNKGVLF 192
Qy      187 HSESGTIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
      193 HLNNEKSFYSYDLFYTGDLGPVSLFKIYEDNKTIIESEKFLHDV 234
```

```
RESULT 34
Q7A4W8 PRELIMINARY; PRT; 242 AA.
ID Q7A4W8
AC Q7A4W8;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin type I.
GN Name=sel; OrderedlocusNames=SA1646;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158879;
```

```
SEQUENCE FROM N.A.
EMBL; AP003364; BAB58170.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bcrt1_tox.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Staph_Strep_toxin; 1.
Pfam; PF02876; Staph_Strep_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN_
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 242 AA; 27863 MW; C5C8BA4CE5414A8 CRC64;
```

```
Query Match 27.4%; Score 339.5; DB 2; Length 242;
Best Local Similarity 35.6%; Pred. No. 6.7e-20;
Matches 79; Conservative 36; Mismatches 74; Indels 33; Gaps 7;
```

```
Qy      23 LSNLRQIY----YNNKAIITENKESDDQFLNTLLFKGFTHGHPWYNDL-LVLDGSKDATN 78
      30 VGNLANFTTKHDYIDLKGVTDKNLPIANGL-----FSTG---TNDLISSNMDEIS 79
Qy      79 KYGKKVDLYGAYYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLMDGKQTV 138
      80 KFKGKKLDIFGIDVNGPC-----KSKYMGATLL-SCQYLNSARKIPINLMWNKHKHTI 132
Qy      139 PIDKVTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQRLIVF 186
      133 STDKATNKGLVTAGQIDVKKRLRYQOEENITIGHNNTGKGEYKSKFYSFNNKGVLF 192
Qy      187 HSESGTIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
      193 HLNNEKSFYSYDLFYTGDLGPVSLFKIYEDNKTIIESEKFLHDV 234
```

RESULT 35

```
Q7A2N9 PRELIMINARY; PRT; 240 AA.
ID Q7A2N9;
AC Q7A2N9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin L.
GN Name=sel; OrderedlocusNames=SAV2008;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_Taxid=158878;
```

```
SEQUENCE FROM N.A.
EMBL; AP003364; BAB58170.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0009405; P:pathogenesis; IEA.
InterPro; IPR008992; Bact_endotox.
InterPro; IPR006177; Bcrt1_tox.
InterPro; IPR006123; Staph/Strep_toxin.
InterPro; IPR006173; Staph_tox_OB.
Pfam; PF01123; Staph_Strep_toxin; 1.
Pfam; PF02876; Staph_Strep_tox_C; 1.
PRINTS; PR00279; BACTRLTOXIN_
PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
Complete proteome.
SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;
```

```
Query Match 27.2%; Score 337; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.1e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;
```

```
Qy      25 NLNRQIY----YNNKAIITENKESDDQFLNTLLFKGFTHGHPWYND-LVLDGSKDATNK 79
      32 NLNRFTYTKRYEYNLKNVNDKNSPESHRL-----YSKNDITLYAFEDNEYITS 80
Qy      80 YGKKKVDLYGAYYGYQACGTPNKTACMYGGVTLHDNNRLTEKKVPINLMDGKQTV 139
      81 LKGNKVDVFGISYK-----GNSRPT--LYGVTVKNNKLDSPRIIPINLIINGHGQTV 134
Qy      140 IDKVTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSGKGVQRLIVF 187
      135 TKSYSTDKWVTAGQIDVKKRLRYQDEFNITIGHNNTGKGEYKSKFYSFNNKGVLF 194
Qy      188 SSEGSTIVSYDLFDAQGYPTDLLRIYRDNKTINSENLHIDL 228
      195 MNDGSNFSYDLFYTGDLGPVSLFKIYEDNKTIIESEKFLHDV 235
```

```
RESULT 36
Q7A4K9 PRELIMINARY; PRT; 240 AA.
ID Q7A4K9;
AC Q7A4K9;
DT 05-JUL-2004 (TREMBlrel. 27, Created)
DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Extracelluluar enterotoxin L.
GN Name=sel; OrderedlocusNames=SA1816;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
```

OK NCBI_TaxID=158879;
 RP [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Iian Y.-Q., Ito T.,
 RA Katsunori M., Matsumaru H., Maruyama A., Murakami H., Hoshoyama A.,
 RA Mizutani-U Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
 RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
 RA Kanehisa M., Yamashita A., Oshino K., Furuya K., Yoshino C., Shiba T.,
 RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,
 RT "Whole genome sequencing of methicillin-resistant *Staphylococcus aureus*."
 RT Lancel 357.1225-1240(2001).
 RU EMBL, AF003135; BAB43096.1; -.
 DR HSSP; P1380; 1AB0.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 27.2%; Score 337; DB 2; Length 240;
 Best Local Similarity 35.3%; Pred. No. 1,1e-19; Indels 34; Gaps 6;
 Matches 78; Conservative 37; Mismatches 72;
 QY 25 NLRLQY----YYNEKATEKESDDQFLNTLLFKGFFTHPWPYND-LIVDLGSKDATNK 79
 DB 32 NLRLFTTKYEVNLYKXVNDKNSPESHRL-----YKNDTLVAEPDNEYITSD 80
 QY 80 YGKQKVDLYGAYGYQCAAGTPNKTCMYGVTLLHNNRLTEKKVPINLMIDGKQTVV 139
 DB 81 LKGNKVDVFGISYK-----GNSRT--YGGVTKAENKLDSPRIIPINLIINGKHQTVV 134
 QY 140 IDKVTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKVGRLIVFH 187
 DB 135 TKSVSSTDKKQVTAQELDVLRKRYLQDEFNLYGHNDTGKGEYGTSSKFGSPDKGSVVFH 194
 QY 188 SSEGSTVSVDLPDAQGYPDTLRLRYDNKNTINSENLHIDL 228
 DB 195 MNDGSNFSYDLPFTYTGGLPESFLIKYDKNTKVDSTQPHLDV 235

RESULT 37
 Q990L7 PRELIMINARY; PRT; 240 AA.
 AC Q990L7;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Sel.
 GN Name=sel.
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2056666; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
 RA Fitzgerald J.R., Monday S.R., Foster T.J., Bonach G.A., Hattigan P.J.,
 RA Meaney W.J., Smyth C.J.;
 RT "Characterization of a putative pathogenicity island from bovine
 RT *Staphylococcus aureus* encoding multiple superantigens."
 RT J. Bacteriol. 183:63-70(2001).
 DR EMBL, AF217235; AAG29598.1; -.

DR PIR; G89991; G89991.
 DR HSSP; Q9R005; 1ET6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
 DR Complete proteome.
 SQ SEQUENCE 240 AA; 27496 MW; F40D62DA73197881 CRC64;

Query Match 27.2%; Score 337; DB 2; Length 240;
 Best Local Similarity 35.3%; Pred. No. 1,1e-19; Indels 34; Gaps 6;
 Matches 78; Conservative 37; Mismatches 72;
 QY 25 NLRLQY----YYNEKATEKESDDQFLNTLLFKGFFTHPWPYND-LIVDLGSKDATNK 79
 DB 32 NLRLFTTKYEVNLYKXVNDKNSPESHRL-----YKNDTLVAEPDNEYITSD 80
 QY 80 YGKQKVDLYGAYGYQCAAGTPNKTCMYGVTLLHNNRLTEKKVPINLMIDGKQTVV 139
 DB 81 LKGNKVDVFGISYK-----GNSRT--YGGVTKAENKLDSPRIIPINLIINGKHQTVV 134
 QY 140 IDKVTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKVGRLIVFH 187
 DB 135 TKSVSSTDKKQVTAQELDVLRKRYLQDEFNLYGHNDTGKGEYGTSSKFGSPDKGSVVFH 194
 QY 188 SSEGSTVSVDLPDAQGYPDTLRLRYDNKNTINSENLHIDL 228
 DB 195 MNDGSNFSYDLPFTYTGGLPESFLIKYDKNTKVDSTQPHLDV 235

RESULT 38
 Q8XKJ5 PRELIMINARY; PRT; 240 AA.
 AC Q8XKJ5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2004 (TrEMBLrel. 22, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE Extracellular enterotoxin L.
 GN Name=se12; Ordered locus names=MM0760;
 OS *Staphylococcus aureus* (strain MM2).
 OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
 OX NCBI_TaxID=196620;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MM2;
 RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08733-5;
 RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
 RA Nagai Y., Iwano M., Amano K., Naito T., Kuroda H., Cui L.,
 RA Yamamoto K., Hiramatsu K.;
 RT "Genome and virulence determinants of high virulence community-
 RT acquired MRSA."
 RT Lancet 359:1819-1827(2002).
 RL EMBL, AP004824; BAB94625.1; -.
 DR HSSP; Q9R005; 1ET6.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR008992; Bact_endotox.
 DR InterPro; IPR006177; Bactl_tox.
 DR InterPro; IPR006123; Staph/Strep_toxin.
 DR InterPro; IPR006126; Staph/Strep_tox.
 DR InterPro; IPR006173; Staph_tox OB.
 DR Pfam; PF01123; Staph_strep_toxin; 1.
 DR Pfam; PF02876; Staph_strep_tox C; 1.
 DR PRINTS; PR00279; BACTRLTOXIN.
 DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
 DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW Complete proteome.
SQ SEQUENCE 240 AA; 27478 MW; 85CD62DA71C3D95 CRC64;
Query Match 27.1%; Score 336; DB 2; Length 240;
Best Local Similarity 35.3%; Pred. No. 1.3e-19;
Matches 78; Conservative 37; Mismatches 72; Indels 34; Gaps 6;
QY 25 NLKQIY---YNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LIVDGSKDATNK 79
DB 32 NLRNRYTKKEYNLKQVNDKNSPESHRL-----YSKNDTLAEFDNEVITSD 80
QY 80 YKGVKVDLYGAYVYQACAGTPTNKACMYGVTLHDNNRLTEKKVPIINLMDGKQTV 139
DB 81 LKGVKVDVFGISYK---GNSRT--YGVVTKAKNNKLDSPRIIPINLILINGKQVTV 134
QY 140 IDKYVTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKAVQRGILVFN 187
DB 135 TKSVSTDKKMTAQAQIDVTKRYQLQDEFNIVGHNTGKCKEYGTSSKFSFGDKSVYFH 194
QY 188 SSEGSTVSVDLFDAGQGYPTTLRIYRDNKTINSENHLIDL 228
DB 195 INDGNSFSYDLPYTGGLPESFLIKYKDKTVDSIQFHLDV 235

RESULT 39
Q8RR75 PRELIMINARY; PRT; 218 AA.
AC Q8RR75;
DT 01-JUN-2002 (TREMBLrel. 21, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin I (Fragment).
DE Enterotoxin I (Fragment).
GN Name=se1;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxId=1280;
RN [1]
RX MEDLINE=2187179; PubMed=11880405;
RA Omeo K., Ishikawa M., Shimoda Y., Hu D.L., Ueda S., Shingawa K.;
RT "Detection of seg, seh, and sei genes in Staphylococcus aureus
isolates and determination of the enterotoxin productivities of S.
aureus isolates harboring seg, seh, or sei genes".
RL J. Clin. Microbiol. 40:857-862(2002).
DR EMBL; AB060537; BAB85991.1; -.
DR HSP; P13380; 1XTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_toxin.
DR Pfam; PF01123; Staph/Strep_toxin; 1.
DR Pfam; PF02876; Staph/Strep_toxin; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 218 AA; 24909 MW; 1017728FB71BF662 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 218;
Best Local Similarity 35.1%; Pred. No. 1.3e-19;
Matches 78; Conservative 37; Mismatches 74; Indels 33; Gaps 7;
QY 23 LSNLRQIY---YNEKAITENKESDDQFLENTLLFKGFFTGHPWYNDLIVDLSKDATN 78
DB 6 VGNLNFYTKHDYIDLKGVTDKPLPIANQLE-----FSTG---TNDLISSENWDEIS 55
QY 79 KYKGVKVDLYGAYVYQACAGTPTNKACMYGVTLHDNNRLTEKKVPIINLMDGKQTV 138
DB 56 KFGKVKLDIFGIDYVGPC-----SKYMFGAATL-SEQYLSARAKIPINLWVNGHKTI 108
QY 139 PIDKYTSKKEVTVQELDLQARHYLHGKFGLYNSDSFG-GK-----VQGLVIF 186
DB 109 STDKTIATNKGLVTAQIDVTKRYQLQDEFNIVGHNTGKCKEYGTSSKFSFGDKSVYFH 168

QY 187 HSSEGSTVSVDLFDAGQGYPTTLRIYRDNKTINSENHLIDL 228
DB 169 HNNKESFSYDLPYTGGLPVSFLIKYEDNKIIESEKPHLDV 210
RESULT 40
Q9L921 PRELIMINARY; PRT; 225 AA.
ID Q9L921;
AC Q9L921;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE 25.7 kDa protein.
OS Streptococcus equi.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
NCBI_TaxId=1336;
RN [1]
RX STRAIN=CF32;
RX MEDLINE=21671707; PubMed=11812213; DOI=10.1006/mpat.2001.0482;
RA Artushin S.C., Timoney J.F., Sheoran A.S., Muthupalan S.K.;
RT "Characterization and immunogenicity of pyrogenic micogens Sepr-H and
Sepr-I of Streptococcus equi".
RL Microb. Pathog. 32:71-85(2002).
DR EMBL; AF16180; AAF72808.1; -.
DR HSP; P13163; 1SXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph/Strep_toxin; 1.
DR Pfam; PF02876; Staph/Strep_toxin; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 225 AA; 25684 MW; EB43D47B26FB9F89 CRC64;

Query Match 27.1%; Score 335.5; DB 2; Length 225;
Best Local Similarity 34.4%; Pred. No. 1.3e-19;
Matches 76; Conservative 42; Mismatches 80; Indels 23; Gaps 6;
QY 25 NLKQIY---YNEKAITENKESDDQFLENTLLFKGFFTGHPWYND-LIVDLSKDATNTYK 81
DB 8 NLRNRYSTYDLPYTGGLPVSFLIKYEDNKIIESEKPHLDV 210
QY 82 GKVVDLYGAYVYQACAGTPTNKACMYGVTLHDNNRLTEKKVPIINLMDG--KQTV 138
DB 64 GKVVDLYGAYVYQACAGTPTNKACMYGVTLHDNNRLTEKKVPIINLMDG--KQTV 119
QY 139 PIDKYTSKKEVTVQELDLQARHYLHGKFGLY-----NSDSFGKAVQRGILVFN 189
DB 120 DLSVSTDKKMTAQAQIDVTKRYQLQDEFNIVGHNTGKCKEYGTSSKFSFGDKSVYFH 179
QY 190 EGSSTVSVDLFDAGQGYPTTLRIYRDNKTINSENHLIDL 230
DB 160 SGERISYVLPFGHGRDSMLKYSNDKNTAVSDQHLIDYL 220

RESULT 41
Q99Z21 PRELIMINARY; PRT; 225 AA.
ID Q99Z21;
AC Q99Z21;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Streptococcal exotoxin I.
GN Name=se1; Ordered locus names=SPY1007;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

```

OC Streptococcus.
RX NCBI_TaxId=1314;
RN
RN SEQUENCE FROM N.A.
RC STRAIN=SF370 / ATCC 700294 / Serotype M1;
RX MEDLINE=21192684; PubMed=11296296; DOI=10.1073/pnas.071559398;
RA Ferretti J.J., Meshan W.M., Ajdic D.J., Savic G., Lyon K.,
RA Primeaux C., Sezate S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,
RA Qian Y., Jia H.G., Najjar F.Z., Ren Q., Zhu H., Song L., White J.,
RA Yuan X., Clifton S.W., Roe B.A., McLaughlin R.E.;
RT "Complete genome sequence of an M1 strain of Streptococcus pyogenes.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).
DR EMBL: AB006546; AK33906.1; -.
DR HSSP: Q9RQ05; 1E76.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endocox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 225 AA; 25611 MW; CE0D6736CC11CC04 CRC64;

Query Match 27.0%; Score 334.5; DB 2; Length 225;
Best Local Similarity 34.4%; Pred. No. 1.6e-19;
Matches 76; Conservative 42; Mismatches 80; Indels 23; Gaps 6;

QY 25 NLRLQIYYNEKAITENKESDDQFLNTLLFKGFFGHPWYN--DLVLDGSDATNKKY 81
DB 8 NLRLNYSTVDPTPEVKKINEGPFSGSLFYKNI---PYGNSISIEHKVELINSYEKANF 63
QY 82 GKRVLDYGAYYGQACAGTPTNKACMYGVTLHDNNRLTEKKVPINLMTDG---KQTV 138
DB 64 GKRVLDFTLEYSPPCSNKNKNS--YGGITLSDGRI-DKNIPVNIPLFDGVQOQKSYT 119
QY 139 PIDKVTSKKEVTVOELDLQARHYLHGKFLY-----NSDSFGKQVQGLIVFHS 189
DB 120 DISTGSTDKKEVTIQLDLVKSRYTLQKHPIYFGDVYKGRGSRKQSGEBENIIFHLN 179
QY 190 EGSIVSYDLFDAGQYPTLLRIYRDNKTINSNLHIDL 230
DB 180 SGERISYVNFDTGHGRSMLKKYSNKNKTAVSQDLHIDVL 220

RESULT 42
Q99T47 PRELIMINARY; PRT; 239 AA.
AC Q99T47;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Enterotoxin.
GN Name=sem; OrderedLocuNames=SAV1829;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158878;
RN
RN SEQUENCE FROM N.A.
RP STRAIN=Mu50 / ATCC 700699;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chii U., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hatakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;

```

```

RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003363; BAB5799.1.1; -.
DR FIR: D8969; D8969.
DR HSSP: Q9RQ05; 1E76.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endocox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph_tox_OB.
DR Pfam: PF01123; Staph_Strep_toxin; 1.
DR Pfam: PF02876; Staph_Strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match 25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 2.7e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRLQIYYNEKAITENK--ESDDQFLNTLLFKGFFGHPWYNDLVLVLDGSDATNKKY 82
DB 28 NLRLN--YGSYPIEDHQINPENNLHQLVFS-----MDNSTVAEFKNVDVKKFYK 79
QY 83 KRVLDYGAYYGQACAGTPTNKACMYGVTLHDNNRLTEKKVPINLMTDGKQTVPIDK 142
DB 80 HAVDVYGLSYGYCL-----KNRYIGVTL-AGDYLEKSRRIPINLWNGEHQITSTK 133
QY 143 VTKSKKEVTVOELDLQARHYLHGKFLY-----NSDSFGKQVQGLIVFHS 190
DB 134 VSTNKKLVTAQELIDTLKRLYLQEBYNIYGFNDTNKRANGNKSPSSGNAGILPLHLD 193
QY 191 GSTVSYDLFDAGQYPTLLRIYRDNKTINSNLHIDL 228
DB 194 GGSFSYDLFDTGQAESFLKIYNDKVTETEFHIDV 231

RESULT 43
Q7A4W7 PRELIMINARY; PRT; 239 AA.
AC Q7A4W7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Enterotoxin SEM.
GN Name=sem; OrderedLocuNames=SA1647;
OS Staphylococcus aureus (strain N315).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=158879;
RN
RN SEQUENCE FROM N.A.
RP STRAIN=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;
RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Chii U., Oguchi A., Aoki K.-I., Nagai Y., Iian J.-Q., Ito T.,
RA Kanamori M., Matsunaru H., Maruyama A., Murakami H., Hosoyma A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hatakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
DR EMBL: AP003363; BAB42915.1; -.
DR HSSP: P1380; 1AN8.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endocox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.

```

```
DR Pfam; PF01123; Scap_Strp_toxin; 1.
DR Pfam; PF02876; Scap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN-.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 239 AA; 27370 MW; 5F29665125705600 CRC64;

Query Match      25.8%; Score 320; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 2.7e-18;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRLQIYYNEKAIYENK--ESDDQPLENTLLFKGFPTGHPWYNDLLVLDGSDATANKYK 82
DB 28 NLRLN--YVGSYPIDHOSINPENNLISHQLVFS-----MDNSTYTAEPKXVDVKKFKN 79
QY 83 KKVLDYGAIVYGQAGGTPNKTACMGVGLTHDNNRLTEEEKVPINLWIDGKQTVPIDK 142
DB 80 HAVDYGLDSYSGYCL-----KKKTYGGVTL-AGDYLEKSRRIPIINLWVNGEHQITISDK 133
QY 143 VKTSKEVTVQELDLQARHYLHGKFGLY-----NSDFGKVGORGLIVFHSSE 190
DB 134 VSTKKVLTAGIEDTKLARIQEEYNIYGFNDTKGRMYGNKSKSGFNNGKILFHLND 193
QY 191 GSTVSYDLFPAQGGYPTDLRLRIYRDNKTINSENHIDL 228
DB 194 GSSFSYDLFDTGTCQAESFLKIYNDNKTIVETEKFHLDV 231

RESULT 44
Q8NVM3 PRELIMINARY; PRT; 242 AA.
AC Q8NVM3;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Staphylococcal enterotoxin Seg.
GN Name=seg2; OrderedLocustNames=WM1937;
OS Staphylococcus aureus (strain MM2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;

RA "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004828; BAB95802.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Scap/Strep_toxin.
DR InterPro; IPR006126; Scap/Strep_tox.
DR InterPro; IPR008375; Scaph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Scap_Strp_toxin; 1.
DR PRINTS; PR00279; BACTRLTOXIN-.
DR PROSITE; PR01800; STAPHHEXOTOXN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28139 MW; FFC089BBOE7A3BF5 CRC64;

Query Match      25.8%; Score 319.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 3e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;
```

```
QY 25 NLRLQIYYNEK--AITENKESDDQPLENTLLFKGFPTGHPWYNDLLVLDGSDATANKY 80
DB 32 NLRLNRYANYQPEKIQGVSSGNFSTSHOLE---YIDGKXTLYSOPH-----NEY 76
QY 81 KGK-----KVLDYGAIVYGQAGGTPNKTACMGVGLTHDNNRLTEEEKVPINLWIDGK 135
DB 77 EAKRLKDKHVDIFGISYGLC-----NTKMYGQITLANON-LDKPNIPIINLWVNGKQ 129
QY 136 TTVPIDKVKTSKKEVTVQELDLQARHYLHGKFGLYN-----SDSFGKVGORGL 183
DB 130 NTISIDKYSTQKKEVTVQELDIDKRLKYLQNEYNINYGFKTKGQGEYKSKFNSGFNGK 189
QY 184 IVFHSSEGSTVSYDLFPAQGGYPTDLRLRIYRDNKTINSENHIDL 228
DB 190 ITFHLNNEPSFTYDLFYTGTCQAESFLKIYNDNKTIDAENFHLDV 234

RESULT 45
Q6G7U1 PRELIMINARY; PRT; 242 AA.
AC Q6G7U1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocustNames=SAS1920;
OS Staphylococcus aureus (strain MSSA476).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=262459;

RA "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571857; CAG31727.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Scap/Strep_toxin.
DR InterPro; IPR006126; Scap/Strep_tox.
DR InterPro; IPR008375; Scaph_exotoxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Scap_Strp_toxin; 1.
DR Pfam; PF02876; Scap_Strp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PR01800; STAPHHEXOTOXN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 242 AA; 28139 MW; FFC089BBOE7A3BF5 CRC64;

Query Match      25.8%; Score 319.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 3e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRLQIYYNEK--AITENKESDDQPLENTLLFKGFPTGHPWYNDLLVLDGSDATANKY 80
DB 32 NLRLNRYANYQPEKIQGVSSGNFSTSHOLE---YIDGKXTLYSOPH-----NEY 76
QY 81 KGK-----KVLDYGAIVYGQAGGTPNKTACMGVGLTHDNNRLTEEEKVPINLWIDGK 135
DB 77 EAKRLKDKHVDIFGISYGLC-----NTKMYGQITLANON-LDKPNIPIINLWVNGKQ 129
```

```

QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYN-----SDSFGKVVQRL 183
DB 130 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYGSKFNSGPNK 189
QY 184 IYFHSSEGSTVSYDLFDAQGYPDTLRLIRYRNKKTINSENLHIDL 228
DB 190 ITFHLNNEPSFTYDLFYTGGAESFLKTYNDNKITIDANFHLDV 234

RESULT 46
QBLVW7 PRELIMINARY; PRT; 256 AA.
ID 08VLW7:
AC 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DE 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Staphylococcus enterotoxin Q.
GN Name=entQ;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RX MEDLINE=9835824; PubMed=9720870;
RA Lindsay J.A., Kuzin A., Ross H.F., Kurepina N., Novick R.P.;
RT "The gene for toxic shock toxin is carried by a family of mobile
  pathogenicity islands in Staphylococcus aureus."
RL Mol. Microbiol. 29:527-543(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RN4282;
RA Barry P.C., Novick R.P.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; U93688; AAL67620.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR Pfam; PF01123; Staphylococcus; IEA.
DR Pfam; PF02876; Staphylococcus; IEA.
DR PRINTS; PR00279; BACTRITOXIN.
DR PRINTS; PR01800; STAPHYLOTOXIN.
DR PROSITE; PS00277; STAPHYLOTOXIN_1; UNKOWN_1.
DR PROSITE; PS00278; STAPHYLOTOXIN_2; 1.
SQ SEQUENCE 256 AA; 29794 MW; 9E2F13790823A7DF CRC64;

Query Match 25.7%; Score 318.5; DB 2; Length 256;
Best Local Similarity 33.8%; Pred. No. 3, 8e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFGHFWYNDLLVDLSKDATNKY 80
DB 46 NLRNFYANPEPELQGVSGNFSHQLB---YIDKYLTYSGFH-----NEY 90
QY 81 KKG-----KYDLYGAYGYQAGTGNKTAQMGVTLHDNNRLTEKKVPINLWIDKQ 135
DB 91 EAKRLDKHVKDIFGISYGLC-----NTKMYGGITLANON-LDKPRNIPINLWNGKQ 143
QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYN-----SDSFGKVVQRL 183
DB 144 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYGSKFNSGPNK 203
QY 184 IYFHSSEGSTVSYDLFDAQGYPDTLRLIRYRNKKTINSENLHIDL 228
DB 204 ITFHLNNEPSFTYDLFYTGGAESFLKTYNDNKITIDANFHLDV 248

RESULT 47
QBLVW7 PRELIMINARY; PRT; 242 AA.
ID 093CC6:
AC 093CC6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)

```

```

DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Seq.
GN Name=seq;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=2193538; PubMed=11821418; DOI=10.1074/jbc.M11661200;
RA Yarwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
  Schlievert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
  pathogenicity island 3. Implications for the evolution of
  staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277:13138-13147(2002).
DR EMBL; AF410775; AAL04146.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR008375; Staph_exotoxin.
DR Pfam; PF01123; Staphylococcus; IEA.
DR Pfam; PF02876; Staphylococcus; IEA.
DR PRINTS; PR00279; BACTRITOXIN.
DR PRINTS; PR01800; STAPHYLOTOXIN.
DR PROSITE; PS00277; STAPHYLOTOXIN_1; UNKOWN_1.
DR PROSITE; PS00278; STAPHYLOTOXIN_2; 1.
SQ SEQUENCE 242 AA; 28184 MW; F6E8F0A4F6C30D85 CRC64;

Query Match 25.6%; Score 316.5; DB 2; Length 242;
Best Local Similarity 33.8%; Pred. No. 5, 2e-18;
Matches 76; Conservative 35; Mismatches 71; Indels 43; Gaps 8;

QY 25 NLRQIY--YYNEK--AITENKESDDQFLENTLLFKGFFGHFWYNDLLVDLSKDATNKY 80
DB 32 NLRNFYANPEPELQGVSGNFSHQLB---YIDKYLTYSGFH-----NEY 76
QY 81 KKG-----KYDLYGAYGYQAGTGNKTAQMGVTLHDNNRLTEKKVPINLWIDKQ 135
DB 77 EAKRLDKHVKDIFGISYGLC-----NTKMYGGITLANON-LDKPRNIPINLWNGKQ 129
QY 136 TTVPIDKVTSSKEVTVQELDQARHYLHGKFGLYN-----SDSFGKVVQRL 183
DB 130 NTISTDKVSTQKEVTAQAEIDIKRLKYLQNEVNIYGFNKKQGEYGYGSKFNSGPNK 189
QY 184 IYFHSSEGSTVSYDLFDAQGYPDTLRLIRYRNKKTINSENLHIDL 228
DB 190 ITFHLNNEPSFTYDLFYTGGAESFLKTYNDNKITIDANFHLDV 234

RESULT 48
QBLVW7 PRELIMINARY; PRT; 239 AA.
ID 09EZM7:
AC 09EZM7;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE SEM.
GN Name=sem;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A900322;
RX MEDLINE=20571956; PubMed=11123352;
RA Jarraud S., Peyrat M.A., Lim A., Tristan A., Bes M., Mougel C.,

```

RA Etienne J., Vandenesch F., Bonneville M., Iina G.,
RT "egc, a highly prevalent operon of enterotoxin gene, forms a putative
RT nursery of superintigens in *Staphylococcus aureus*."
RL J. Immunol. 166:669-677(2001).
DR EMBL; AF285760; AAG36952.1; -.
DR HSSP; Q9R0Q5; 1E76.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 239 AA; 27371 MW; 69240BE23C44028A CRC64;

Query Match 25.5%; Score 316; DB 2; Length 239;
Best Local Similarity 32.6%; Pred. No. 5.7e-18;
Matches 71; Conservative 41; Mismatches 78; Indels 28; Gaps 6;

QY 25 NLRLQYYNEKATINENK--ESDDQFLENTLLFKGFFTGHPWYNDLVLDGSKDATNKYKG 82
DB 28 NLRL--YGGYPTEHQSIENPNHLSHQLVFS-----MDNSTVAEFKVDVKEFKN 79
QY 83 KVDLYGAYYGQACGTPNKTACMYGVTLDHNNRLTEKKVPINLMDGKQTTVPIDK 142
DB 80 HAVDVYGSYGCL-----KKKTYIGGVTL-AGYILKSRRIPIINLVNGEHQIISIDK 133
QY 143 VKTSKEVTVQELDQARHYLHGKFGLY-----NSDFGKVGQRLVFSHS 190
DB 134 VSTNKKVLTQAEIDTKRLRYQEEFNIVGFNDTNKGRVYGNKSPSGFNAGKILFHLND 193
QY 191 GSTVSYDLFDAGQYPTLLRIYRNKNTINSENHLIDL 228
DB 194 GSSPSYDLFTGTGQAESFLKTYNDKTYETKEFHLDV 231

RESULT 49

ID Q711S9 PRELIMINARY; PRT; 86 AA.
AC Q711S9;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Putative enterotoxin (Fragment).
OS *Staphylococcus intermedius*.
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.
RA Becker K.;
RL Theiss (2001), Department of Institute of Medical Microbiology,
RL University of Muenster, Muenster, Germany.
DR EMBL; AJ307889; CAC86191.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
FT NON TER 86
SQ SEQUENCE 86 AA; 9877 MW; 21C191E65EAF72AC CRC64;

Query Match 25.2%; Score 312; DB 2; Length 86;
Best Local Similarity 66.3%; Pred. No. 3.5e-18;
Matches 57; Conservative 15; Mismatches 14; Indels 0; Gaps 0;

QY 127 INLWMDGQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGVNSDFGKVGQRLVIF 186
DB 1 VNLWMDGQTTVPIDKVKTSKEVTVQELDQARHYLHGKFGVNSDFGKVGQRLVIF 60

QY 187 HSSGTSVSYDLFDAGQYPTLLRI 212
DB 61 ETSRSHSASVYDLAAEGKADTIIRI 86

RESULT 50

ID Q8NVW2 PRELIMINARY; PRT; 242 AA.
AC Q8NVW2;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE *Staphylococcus enterotoxin* Sek.
GN Name=sek2; OrderedLocNames=MM1938;
OS *Staphylococcus aureus* (strain MM2).
OC Bacteria; Firmicutes; Bacillales; *Staphylococcus*.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MM2;
RX MEDLINE=22040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda M., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naimi T., Kuroda H., Cui L.,
RA Yanamoto K., Hiramatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004828; BAB95803.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 242 AA; 27848 MW; FC377CB4C9BBB4E3 CRC64;

Query Match 25.0%; Score 310; DB 2; Length 242;
Best Local Similarity 33.2%; Pred. No. 1.8e-17;
Matches 74; Conservative 39; Mismatches 76; Indels 34; Gaps 9;

QY 23 LSNLRQIY----YNEKATINENKESDDQFLENTLLFKGFFTGHPWYNDLVLDGSKDATN 78
DB 29 IDNLNENFTYTKDFINLKVKN---DTPINQLOP-----SNSY-DLISESKDPNFKFS 78
QY 79 KYGKGVLDYGAAYGYQCAGTGNKTACMYGVTLDHNNRLTEKKVPINLMDGKQTTV 138
DB 79 NFKGKGLDVFGISVNGC-----NTKTYIGGVTL-TREYLDKRNIPINLVINGNHKTI 131
QY 139 PIDKVKTSKEVTVQELDQARHYLHGKFGLY-----NSDFGKVGQRLVIF 186
DB 132 STNKKVSTNKKVTVQAEIDTKRLRYQEEFNIVGFNDTNKGRVYGNKSPSGFNAGKILFHLND 191
QY 187 HSSGTSVSYDLFDAGQYPTLLRIYRNKNTINSENHLIDL 228
DB 192 HLNNDFTSYDLFTGTGDDGLPKSFLKTYEDNKTYESEKFLHDV 234

RESULT 51

ID Q6G7U0 PRELIMINARY; PRT; 242 AA.
AC Q6G7U0;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocNames=SA51921;
OS *Staphylococcus aureus* (strain MSSA476).

[illegible]

```

RESULT 53
054476 PRELIMINARY; PRT; 242 AA.
ID 054476
AC 054476;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin K.
GN Name=entK;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RM4282;
RX MEDLINE=96385624; PubMed=9720870;
   Lindaay J.A., Rubin A., Ross H.F., Kurepina N., Novick R.P.;
RT "The gene for toxic shock toxin is carried by a family of mobile
   pathogenicity islands in Staphylococcus aureus.";
RL Mol. Microbiol. 29:527-543(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=RM4282;
RX Barry P.C., Novick R.P.;
RT Submitted (JAN-2002) to the EMBL/Genbank/DBJ databases.
DR EMBL; U93688; AAC28968.1; -.
DR HSP; P1380; IKTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00378; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA, 27720 MW, 28CB4F2EE686B9 CRC64;

```

```
Query Match      25.0%; Score 309; DB 2; Length 242;
Best Local Similarity 32.9%; Pred. No. 2.2e-17;
Matches 72; Conservative 40; Mismatches 81; Indels 26; Gaps 7;

QY 23 LSNLRQIYYNEKATENKESDDQFLIENTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYK 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 29 IDNLRNFYTKDIPVDLKVDKONDPTPIANQLQF-----SNESY-DLISSEKDPNKSFNKG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAIVYGQACGATPNTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 83 KKLDFVFGISYNGQC-----NTKYIYGVTATNRYLDKSRNIPINIMINGNHKTIISTNK 135
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTQVELDQARHYLHGKFGLY-----NSDFGCK-----VQGLIVFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 136 VSTNKKLVTAQEBIDVKLRKYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLHNN 195
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLF-DAQGYPDTLRIYRDNKTINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGGDGLPKSPFKIYEDNKTVESEKPHLDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 54
Q93CC5 PRELIMINARY; PRT; 242 AA.
AC Q93CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sek.
GN Name=sek;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M11661200;
  Yawwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
  Schlevert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
  pathogenicity island 3. Implications for the evolution of
  staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277.13138-13147(2002).
DR EMBL; AF410775; AAL04147.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006173; Staph_Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTRILOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B99D9C9A9A CRC64;

Query Match      25.0%; Score 309; DB 2; Length 242;
Best Local Similarity 32.9%; Pred. No. 2.2e-17;
Matches 72; Conservative 40; Mismatches 81; Indels 26; Gaps 7;

QY 23 LSNLRQIYYNEKATENKESDDQFLIENTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYK 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 29 IDNLRNFYTKDIPVDLKVDKONDPTPIANQLQF-----SNESY-DLISSEKDPNKSFNKG 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAIVYGQACGATPNTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 83 KKLDFVFGISYNGQC-----NTKYIYGVTATNRYLDKSRNIPINIMINGNHKTIISTNK 135
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTQVELDQARHYLHGKFGLY-----NSDFGCK-----VQGLIVFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 136 VSTNKKLVTAQEBIDVKLRKYLQEEYNIYGHNGTKGGEYGHKSKFYSGFNIGKVTFLHNN 195
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLF-DAQGYPDTLRIYRDNKTINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGGDGLPKSPFKIYEDNKTVESEKPHLDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 54
Q93CC5 PRELIMINARY; PRT; 242 AA.
AC Q93CC5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Sek.
GN Name=sek;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COL;
RX MEDLINE=21935388; PubMed=11821418; DOI=10.1074/jbc.M11661200;
  Yawwood J.M., McCormick J.K., Paustian M.L., Orwin P.M., Kapur V.,
  Schlevert P.M.;
RT "Characterization and expression analysis of Staphylococcus aureus
  pathogenicity island 3. Implications for the evolution of
  staphylococcal pathogenicity islands."
RL J. Biol. Chem. 277.13138-13147(2002).
DR EMBL; AF410775; AAL04147.1; -.
DR HSSP; P13380; 1KTK.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006173; Staph_Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTRILOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 242 AA; 27727 MW; 207938B99D9C9A9A CRC64;
```

```
QY 191 GSTVSYDLF-DAQGYPDTLRIYRDNKTINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 196 NDTFSYDLFYTGGDGLPKSPFKIYEDNKTVESEKPHLDV 234
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 55
Q9GFM8 PRELIMINARY; PRT; 239 AA.
ID Q9GFM8;
AC Q9GFM8;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterococin.
GN OrderedLocustNames=SAR1920;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=262458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnae.0402521101;
  Holden M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
  Enright M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
  Baeson N., Bentley S.D., Chillingworth C., Chillingworth T.,
  Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Doud L.,
  Fellwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jørgensen K.,
  James K.D., Kennard N., Lane A., Mayes R., Mouton K.,
  Ormond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
  Sharp S., Simmonds M., Stevens K., Whitehead S., Barrall B.G.,
  Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
  evidence for the rapid evolution of virulence and drug resistance."
RT Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40906.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_tox.
DR InterPro; IPR006173; Staph_Strep_toxin.
DR InterPro; IPR006173; Staph_tox OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C_1.
DR PRINTS; PR00279; BACTRILOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR KW Complete proteome.
SQ SEQUENCE 239 AA; 27410 MW; 7AABCTAEAFCA3FBB CRC64;

Query Match      24.4%; Score 302; DB 2; Length 239;
Best Local Similarity 33.0%; Pred. No. 8.1e-17;
Matches 72; Conservative 40; Mismatches 78; Indels 28; Gaps 7;

QY 25 NLKQIYYNEKAIT--ENKESDDQFLIENTLLFKGFFTGHPWYNDLLVLDGSKDATTNKYK 82
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 28 NLRN--YGSYPIEDHONINPDNNRLSHQVFS-----KNSYTAFAKVEDYKFKEN 79
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 83 KKVLDYGAIVYGQACGATPNTACMYGGVTLHDNNRLTEKKVPINLWIDGKQTTVPIDK 142
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 80 RAVDVSGLSYSGYCL-----NKRYMGVTL-AGDYLEKSRICIPINLWVNSGLKTISTDK 133
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 143 VKTSKKEVTQVELDQARHYLHGKFGLYNSD-----SFGK-----VQGLIVFHSSE 190
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 134 VSTNKKLVTAQEBIDVKLRKYLQEEYNIYGHNGTKGGRYGTGSKFYSGFNIGKVTFLHNN 193
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

QY 191 GSTVSYDLFDAQGYPDTLRIYRDNKTINSENLHIDL 228
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :
DB 194 GTSFSYDLFDGTGQABESFLKIYDNKTKVERDVKPHLDV 231
   ||||| : : : : : ||||| : : : : : ||||| : : : : : ||||| : : : : :

RESULT 56
ETX8 STAU
ID ETX8 STAU
AC P01552;
DT 21-JUL-1986 (rel. 01, Created)
```

DT 13-AUG-1987 (Rel. 05, Last sequence update)
 DE 25-OCT-2004 (Rel. 45, Last annotation update)
 DR Enterotoxin type B precursor (SEB).
 GN Name=entB;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 ON NCBI_TaxId=1280;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=86168029; PubMed=3957869;
 RA Jones C.L., Khan S.A.;
 RT "Nucleotide sequence of the enterotoxin B gene from Staphylococcus aureus."
 RL J. Bacteriol. 166:29-33(1986).
 RN [2]
 RP SEQUENCE OF 40-91 FROM N.A.
 RX MEDLINE=85298255; PubMed=3898073;
 RA Rameil D.M., Jones C.L., Johns M.B., Musey G.J., Khan S.A.;
 RT "Molecular cloning of staphylococcal enterotoxin B gene in Escherichia coli and Staphylococcus aureus."
 RL Proc. Natl. Acad. Sci. U.S.A. 82:5850-5854(1985).
 RN [3]
 RP SEQUENCE OF 28-266 (S-6).
 RX MEDLINE=71007902; PubMed=5470821;
 RA Huang I.-Y., Bergdoll M.S.;
 RT "The primary structure of staphylococcal enterotoxin B. 3. The cyanogen bromide peptides of reduced and aminoethylated enterotoxin B, and the complete amino acid sequence."
 RL J. Biol. Chem. 245:3518-3525(1970).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
 RX MEDLINE=93063291; PubMed=1436058; DOI=10.1038/359801a0;
 RA Swaminathan S., Purey W.F. Jr., Pletcher J., Sax M.;
 RT "Crystal structure of staphylococcal enterotoxin B, a superantigen."
 RL Nature 359:801-806(1992).
 RN [5]
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF COMPLEX WITH MHC II.
 RX MEDLINE=94203282; PubMed=8152483; DOI=10.1038/368711a0;
 RA Jardetzky T.S., Brown J.H., Gorga J.C., Stern L.J., Urban R.G., Chli Y.I., Stauffer C., Strominger J.L., Wiley D.C.;
 RT "Three-dimensional structure of a human class II histocompatibility molecule complexed with superantigen."
 RL Nature 368:711-716(1994).
 RN [6]
 RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) OF COMPLEX WITH TCR.
 RX MEDLINE=99096298; PubMed=9881971; DOI=10.1016/S1074-7613(00)80646-9;
 RA Li H., Ilera A., Tsuchiya D., Leder L., Ysern X., Schlievert P.M., Karjalainen K., Mariuzza R.A.;
 RT "Three-dimensional structure of the complex between a T cell receptor beta chain and the superantigen staphylococcal enterotoxin B."
 RL Immunity 9:807-816(1998).
 RN [7]
 RP X-RAY CRYSTALLOGRAPHY (1.5 ANGSTROMS).
 RX MEDLINE=98181012; PubMed=9514739; DOI=10.1006/jmbi.1997.1577;
 RA Papageorgiou A.C., Tranter H.S., Acharya K.R.;
 RT "Crystal structure of microbial superantigen staphylococcal enterotoxin B at 1.5-A resolution: implications for superantigen recognition by MHC class II molecules and T-cell receptors."
 RL J. Mol. Biol. 277:61-79(1998).
 CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.ebi.ac.uk/announcements>)

CC or send an email to license@sib.ch.
 CC -----
 DR EMBL: M1118; AAA8550.1; -.
 DR PIR: S27360; ENSAB6.
 DR PDB: 1D5M; X-ray; C=28-266.
 DR PDB: 1D5X; X-ray; C=28-266.
 DR PDB: 1D5Z; X-ray; C=28-266.
 DR PDB: 1D6E; X-ray; C=28-266.
 DR PDB: 1SBB; X-ray; B/D=28-266.
 DR PDB: 1SR3; X-ray; @=28-266.
 DR PDB: 1SR4; X-ray; @=28-266.
 DR PDB: 1SEB; X-ray; D/H=29-262.
 DR PDB: 2SEB; X-ray; D=28-266.
 DR PDB: 3SEB; X-ray; @=28-265.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006123; Bactl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR Pfam: PF02876; Staph_Strep_tox_C; 1.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW 3D-structure; Direct protein sequencing; Enterotoxin; Signal;
 KW Superantigen; Toxin.
 FT SIGNAL 1..27
 FT CHAIN 28..266
 FT DISULFID 120..140
 FT CONFLICT 56..58
 FT CONFLICT 69..77
 FT CONFLICT 118..118
 FT CONFLICT 128..130
 FT CONFLICT 133..135
 FT CONFLICT 149..150
 FT CONFLICT 156..156
 FT CONFLICT 185..186
 FT CONFLICT 233..233
 FT CONFLICT 246..247
 FT STRAND 29..29
 FT HELIX 41..43
 FT STRAND 44..44
 FT TURN 48..48
 FT HELIX 49..52
 FT HELIX 53..55
 FT STRAND 60..66
 FT STRAND 69..69
 FT TURN 73..74
 FT STRAND 75..78
 FT TURN 83..85
 FT STRAND 90..94
 FT HELIX 98..104
 FT TURN 105..106
 FT STRAND 108..113
 FT STRAND 116..116
 FT TURN 118..119
 FT TURN 127..128
 FT STRAND 138..142
 FT STRAND 145..147
 FT TURN 149..150
 FT STRAND 152..155
 FT TURN 166..167
 FT STRAND 168..179
 FT STRAND 181..183
 FT HELIX 184..199
 FT STRAND 209..218
 FT TURN 219..220
 FT STRAND 221..226
 FT STRAND 232..232
 FT HELIX 237..241
 FT STRAND 242..246
 FT TURN 249..251
 FT TURN 252..254

[illegible]

```

Db      KTCWVGATVEHDGNDIDKKNSTDNSHNLTIKVFEINERSLSFPD-IPTNKKIT7AQOEIDYK 186
Qy      159 ARHYLHGKRGCLYNDSFGKGVRGLIVHSSSGTSVSDLPDAQO--YPDTLLRIYRDN 216
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      VRYNYLLKHKNLVIEFNS--SPYETGYIKFIENGHSFWYDMMPESGEKFFPYTKILLIYNDN 244
Qy      217 KTINSENLAIDLVL 230
       |||::|::::::::::|
Db      245 KTVESKSINVEVHL 258

RESULT 58
QGEGFN0
ID QGEGFN0 PRELIMINARY; PRT; 261 AA.
AC OGGFN0;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedlocusNames=SAR1918;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcuss.
OX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Highten M.T.G., Fell E.J., Lindsay J.A., Peacock S.J., Day N.P.J.,
RA Erdington M.C., Foster T.J., Moore C.E., Hurst L., Atkin R., Barron A.,
RA Basson N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Deggett J., Dowd L.,
RA Feltwell T., Hance Z., Harris B., Hauser H., Holroyd S., Jagels K.,
RA James K.D., Lennard N., Line A., Mayes R., Moule S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S.G., Simmonds M., Stevens K., Whitehead S., Barrett B.G.,
RA Spratt B.G., Parkhill J.;
RL "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL; BX571856; CAG40904.1;-
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endocox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006123; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strept_toxin; 1.
DR Pfam; PF02876; Staph_strept_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREPT_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREPT_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 261 AA; 30547 MW; A407E960CC5974B0 CRC64;

Query Match 24.1%; Score 298; DB 2; Length 261;
Best Local Similarity 31.5%; Pred No. 1,9e-16;
Matches 80; Conservative 49; Mismatches 79; Indels 46; Gaps 133
Db      3 KSEINEKDLRKKSELJORNALSNLRQIIYYNEKAITE-NKESDOFLENTLLFKGFPTGH 61
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      25 KPRLQL-----KASEP-TGLMDNMK--YLDDKHVSEINIRAKOEGLDHDLFFK----- 70
Qy      62 PWYNDLLVDLGSK-----DATNNKYKGVLDYGAVYGYOCAGGTPN-----K 103
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      71 --INGSKIP-GSKILKTPEFNNSSLDKYKNKIUIDFGNYYOOCFPSADNNELNDGLTIE 127
Qy      104 TACMGVGTLEHDNRRLTEEKV--PINMI---DGKOTVPIDKVYSKEKVTVOELDLQ 156
Db      128 KTCMVGATVEHDNQDKKNSTDNSHNLTIKVFEINERSLSFPD-IPTNKKIT7AQOEIDYK 186
Qy      159 ARHYLHGKRGCLYNDSFGKGVRGLIVHSSSGTSVSDLPDAQO--YPDTLLRIYRDN 216
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db      VRYNYLLKHKNLVIEFNS--SPYETGYIKFIENGHSFWYDMMPESGEKFFPYTKILLIYNDN 244
Qy      217 KTINSENLAIDLVL 230
       |||::|::::::::::|
Db      245 KTVESKSINVEVHL 258

```

```

QY      217 KTINSENLHIDLVL 230
DB      245 KTVESKSIIVEVHL 258

RESULT 59
SPEA STRP8 STANDARD; PRT; 251 AA.
ID   SPEA STRP8
AC   P62561; P08095;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE   (SPE A).
GN   Name=speA; OrderedLocusNames=spym18_0393;
OS   Streptococcus pyogenes (serotype M18).
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxId=186103;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=MGAS8232 / Serotype M18;
RX   PubMed=11917108; DOI=10.1073/pnas.062526099;
RA   Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA   Sylva G.L., Sturdevant D.E., Ricklefs S.M., Porcella S.F.,
RA   Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA   Kapur V., Daly J.A., Veary L.G., Musser J.M.;
RT   "Genome sequence and comparative microarray analysis of serotype M18
RT   group A Streptococcus strains associated with acute rheumatic fever
RT   outbreaks";
RT   Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC   -1- FUNCTION: Causative agent of the symptoms associated with scarlet
CC   fever, have been associated with streptococcal toxic shock-like
CC   disease and may play a role in the early events of rheumatic fever
CC   (by similarity).
CC   -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC   chain (by similarity).
CC   -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC   family.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; AE009982; ALU97141.1; -.
CC   DR   InterPro; IPR0068992; Bact_endotox.
CC   DR   InterPro; IPR0061177; Bact_Tox.
CC   DR   InterPro; IPR006123; Staph/Strep_toxin.
CC   DR   InterPro; IPR006126; Staph/Strep_tox.
CC   DR   InterPro; IPR006173; Staph_tox_OB.
CC   pfam; PF02876; Staph_Strep_toxin; 1.
CC   pfam; PF01123; Staph_Strep_toxin; 1.
CC   PRINTS; PR00279; BACTRITOXIN.
CC   DR   PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
CC   DR   PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
CC   Complete proteome; Signal; Toxin.
CC   FT   SIGNAL 1 30 By similarity.
CC   FT   CHAIN 31 251 Exotoxin type A.
CC   FT   DISULFID 117 128 By similarity.
CC   SQ   SEQUENCE 251 AA; 29246 MW; 54001FE4CCBFC3 CRC64;

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best local similarity 34.2%; Pred. No. 2,9e-16;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY      4 SEINEKDLRKSKSELOHNL-SNLRQIYY-YNEKAIT-ENKESDDQPLENTLLFKGFTTG 60
DB      25 SQEVFAQODPDPSQLHSSSLVKNLQNIYFPEYGPVTHENVKSVQDLTSHDLIYN--VS 81

```

```

QY      61 HFWYDLDVLDGSKATNTKRGKVDLYGAYGYGOC-AGCTNKTACWYGVTLHDNNRL 119
DB      82 GNNYDKLKTLELNQEMATLFDKQNVDIYGEVYHLCYLCENERSACTIGVYTNHGNHL 141
QY      120 TEKKVPINLWDIGQTVIPIDKVTSKKEVVOEILDARHYLKGKFGLYNSDSFGKRY 179
DB      142 EIPKTIIVKVSIDGLO-SLSFD-IETNKKMTVAQELDIYVRKYLIDNKQLYNNGP--SKY 197
QY      180 QRGILVFHSSSEGSTVSYDLFD---AGQGYPTLLRIYRDNKTINSENLHIDLVL 232
DB      198 EGVYIKFIPKKNESFWPDEFPEPEFTQSKY----LMIYDNEITLDSNTSQIEVLYLT 250

RESULT 60
SPEA STRPY STANDARD; PRT; 251 AA.
ID   SPEA STRPY
AC   P62560; P08095;
DT   01-AUG-1988 (Rel. 08, Created)
DT   01-JAN-1990 (Rel. 13, Last sequence update)
DT   25-OCT-2004 (Rel. 45, Last annotation update)
DE   Exotoxin type A precursor (Scarlet fever toxin) (Erythrogenic toxin)
DE   (SPE A).
GN   Name=speA;
OS   Streptococcus pyogenes.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxId=1314;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86166804; PubMed=3514452;
RA   Weeks C.R., Ferretti J.D.;
RT   "Nucleotide sequence of the type A streptococcal exotoxin
RT   (erythrogenic toxin) gene from Streptococcus pyogenes bacteriophage
RT   T12.";
RL   Infect. Immun. 52:144-150(1986).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=86284313; PubMed=3526093;
RA   Johnson L.P., L'Italien J.U., Schlievert P.M.;
RT   "Streptococcal pyrogenic exotoxin type A (scarlet fever toxin) is
RT   related to Staphylococcus aureus enterotoxin B.";
RL   Mol. Gen. Genet. 203:354-356(1986).
RN   [3]
RP   X-RAY CRYSTALLOGRAPHY (2.57 ANGSTROMS).
RX   MEDLINE=99094887; PubMed=9878045; DOI=10.1093/emboj/18.1.9;
RA   Papageorgiou A.C., Collins C.M., Gutman D.M., Kline J.B.,
RA   O'Brien S.M., Tranter H.S., Acharya K.R.;
RT   "Structural basis for the recognition of superantigen streptococcal
RT   pyrogenic exotoxin A (SpeA) by MHC class II molecules and T-cell
RT   receptors.";
RL   EMBO J. 18:9-21(1999).
CC   -1- FUNCTION: Causative agent of the symptoms associated with scarlet
CC   fever, have been associated with streptococcal toxic shock-like
CC   disease and may play a role in the early events of rheumatic
CC   fever.
CC   -1- SUBUNIT: Binds to major histocompatibility complex class II beta
CC   chain.
CC   -1- MISCELLANEOUS: This toxin seems to be coded by bacteriophage T12.
CC   -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC   family.
CC   -----
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   -----
CC   EMBL; U40453; AAC48868.1; -.
CC   DR   EMBL; X03929; CA27568.1; -.
CC   DR   PIR; A26152; A26152.
CC   PDB; 1B12; X-ray; -.

```

```
DR PDB; 1FNU; X-ray; --
DR PDB; 1FNU; X-ray; --
DR PDB; 1FNU; X-ray; --
DR PDB; 1H45; X-ray; --
DR PDB; 1LOX; X-ray; --
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Signal; Toxin.
FT SIGNAL 1 30
FT CHAIN 31 251
FT DISULFID 117 128
FT CONFLICT 6 6
FT CONFLICT 17 18
FT CONFLICT 25 35
FT CONFLICT 40 40
FT CONFLICT 43 43
FT CONFLICT 47 59
FT CONFLICT 129 129
FT CONFLICT 165 178
FT TURN 36 38
FT HELIX 42 44
FT TURN 46 48
FT HELIX 49 56
FT STRAND 60 65
FT STRAND 69 74
FT TURN 73 78
FT STRAND 75 78
FT STRAND 82 82
FT TURN 83 84
FT STRAND 85 85
FT STRAND 87 91
FT HELIX 95 102
FT TURN 103 103
FT STRAND 106 110
FT STRAND 113 113
FT TURN 115 116
FT TURN 121 122
FT STRAND 126 130
FT STRAND 133 135
FT TURN 137 138
FT STRAND 140 153
FT TURN 154 155
FT STRAND 156 167
FT STRAND 169 171
FT HELIX 172 186
FT STRAND 197 205
FT STRAND 212 215
FT HELIX 224 227
FT HELIX 228 231
FT TURN 232 233
FT STRAND 236 238
FT TURN 239 241
FT STRAND 243 251
SQ SEQUENCE 251 AA; 29246 MW; 54001FB4CCBCFC3 CRC64;

Query Match 23.9%; Score 295.5; DB 1; Length 251;
Best Local Similarity 34.2%; Pred. No. 2.9e-16;
Matches 81; Conservative 45; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEETNEKLRKSELRNAL-SNLQIYY-VNEKAIT-ENKSDQOFLNTLLFKGFFLG 60
DB 25 SOEVFAQDDPDSQLHRSSLVNLQNIYFLVYGBDVTHENVKSVQQLSHDLIYN---VS 81
```

```
QY 61 HPWYNDLLVDIGSDATITKYGKVDLYGAYYQC-AGTPTNKTACMYGVTILHDNRL 119
DB 82 GPNYDKLTBLKNOEMATLFDKXVDYGVYHLCYLCEAERSACIYGVVTHNEGHL 141
QY 120 TEEKVPINLWIDGQOTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFGSKV 179
DB 142 EIPKIVKVSIDGIQ-SLSFD-IETNKMVTAQELDYKAKYILTDNKQLYTNGP--SKY 197
QY 180 QRLIVFHSSEGSTVSYDLPD---AQGYPTLLRIYRDNKTINSENLHIDLPLYT 232
DB 198 ETGYIKKFIIPKNKESWPFPEPEPTQSKY----LMYKONETLDSNTSQLEVLTYT 250

RESULT 61
Q6RIY7 PRELIMINARY; PRT; 177 AA.
ID Q6RIY7
AC Q6RIY7
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Enterotoxin type M variant (Fragment).
OS Staphylococcus aureus subsp. aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=46170;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 19095;
RX PubMed=1513181;
RA Sergeev N., Volokhov D., Chiznikov V., Rasooly A.;
RT "Simultaneous analysis of multiple staphylococcal enterotoxin genes by
RT an oligonucleotide microarray assay.";
RL J. Clin. Microbiol. 42:2134-2143(2004).
DR EMBL; AY518772; AAR9712.1; -.
DR HSSP; P13380; 1AN8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1 177
FT NON_TER 1 177
SQ SEQUENCE 177 AA; 20215 MW; C6CCD70E5D7B3443 CRC64;

Query Match 23.8%; Score 295; DB 2; Length 177;
Best Local Similarity 37.7%; Pred. No. 2.1e-16;
Matches 61; Conservative 31; Mismatches 52; Indels 18; Gaps 4;

QY 79 KYGKGVLYGAYYQCAAGTPTNKTACMYGVTILHDNRLTEEKVPINLWIDGQOTV 138
DB 22 KFKNRAVDVYGLSYSGYL-----KNKMYGVTIL-AGDYLEKSRCTIPINLWVGNHRTI 75
QY 139 PIDKVTSKKEVTVOELDQARHYLHGKFGLYNSD-----SFGK-----VQGLIVF 186
DB 76 STDKYSTNKKIYVTAQELDTKARLYQSEYNTYGRNDTKGKNGYKSKFSGFNTGKISF 135
QY 187 HSSEGSTVSYDLPDAGQGYPTLLRIYRDNKTINSENLHIDL 228
DB 136 HUNDGTSFSDLPDTGTQGAESFLKIYDNDKVTETDKFHLDV 177

RESULT 62
Q6K6K5 PRELIMINARY; PRT; 251 AA.
ID Q6K6K5
AC Q6K6K5; 079X26;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Enterotoxin type A- phage associated (SpeA precursor).
```

```
GN Name=spea3; OrderedLocName=SP0560; SPYM3_1301;
OS Streptococcus pyogenes (serotype M3);
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus;
OX NCBI_TaxId=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS315 / Serotype M3;
RX MEDLINE=22133808; PubMed=12122206; DOI=10.1073/pnas.152298499;
RA Beres S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
RA Schlievert P.M., Musser J.M.;
RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
RT phage-encoded toxins, the high-virulence phenotype, and clone
RT emergence."
RT Proc. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shiba T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
RT large-scale genomic rearrangement in invasive strains and new insights
RT into phage evolution."
RT Genome Res. 13:1042-1055(2003).
RN [3]
RX EMBL; AE014161; AM79908.1; -;
DR EMBL; AP005142; BAC63655.1; -;
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SER.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Complete proteome.
SQ SEQUENCE 251 AA; 29260 MW; 05E782CDA01BFCD5 CRC64;

Query Match 23.8%; Score 294.5; DB 2; Length 251;
Best Local Similarity 33.8%; Pred. No. 3.6e-16;
Matches 80; Conservative 46; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEINEKDLRKSELOALNLSNLRQIYY-YNKAIT-ENKESDDPLENTLLFKGPFRTG 60
DB 25 SQEVEFAQOPDPSQLRRSSLVKVLQNIYLFEGDPVTHENVKSVDDLLSHDLIYN--VS 81
QY 61 HPTWYNDLVLDGSKATNKYKGVLDYGAHYGQC-AGSTPKTKTCMTGVTLHDNNRL 119
DB 82 GPNYDGLKTELKNOEWALFKDKNIDYGVYVYHLCYLCENARSACTYGGVYTNHGNHL 141
QY 120 TEKKVPIMLMIDGKQTTVPIDKVTSKKEVTVQELDLQARHVLHGFGVYNSDSFGKY 179
DB 142 ETPKTIIVKVSIDGIG-SLSPD-IEITKKNVTAQELDYKVRKYLTDNKKQLYTNGP--SKY 197
QY 180 QRGILVHSHSEGSSTVSYDLFD---AQGOYPTLLRIYRDNKTINSENLHIDLVLVT 232
DB 198 EGVYIKFIPKNKSGFMFDFPPEPFEFQSKX---LMIYKDNELTDSNTSQIEVYLT 250

RESULT 63
Q6XXM3 PRELIMINARY; PRT; 261 AA.
AC Q6XXM3;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
```

```
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DR 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin Seu.
GN Name=seu;
OS Staphylococcus aureus
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=383F;
RX MEDLINE=22692404; PubMed=12807452;
RA Leterrier C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin seu encoded by the egc
RT cluster of Staphylococcus aureus."
RT J. Appl. Microbiol. 95:38-43(2003).
RL J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY205307; AAP41903.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 261 AA; 30535 MW; 663B52AF13794877 CRC64;

Query Match 23.5%; Score 291.5; DB 2; Length 261;
Best Local Similarity 31.0%; Pred. No. 6.6e-16;
Matches 74; Conservative 50; Mismatches 90; Indels 25; Gaps 9;

QY 10 KDLRKSELOALNLSNLRQIYYNKAITE-NKESDDPLENTLLFKGPFRTGHPWYNDLL 68
DB 27 EQLNKASEPS-GLMDNR--YVDDKAVSETIKQAQEKTLQIDLFLKNGSKIDSKILK 83
QY 69 VDLGSKDATNKYKGVLDYGAHYGYCAGTPTN-----KTACMTGGVTLHDNNRL 119
DB 84 TEFNNKSLSDKXKKNKVVDFGTNYVQCYSADNNEMLNDGRLLIEKTCMTGGVTEHDGNOI 143
QY 120 TEKK-----KVPINIMIDGKQTTVPIDKVTSKKEVTVQELDLQARHVLHGFGVYNSD 173
DB 144 DKNNLTDNSHNLIKYV-ENERTLSFD-ISTNMKNITQOEIDYKVRNVLKRNKLYERN 201
QY 174 SFGKQVGRGLIVFHSSEGSSTVSYDLFDAQGO--YPTLLRIYRDNKTINSENLHIDLVL 230
DB 202 S--SPYSGYIKFIEGNSHFWYDMMPSEGEKFTYKYLITNDKTVSKSINVEVHL 258

RESULT 64
Q6XXM5 PRELIMINARY; PRT; 261 AA.
AC Q6XXM5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin Seu.
GN Name=seu;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=352B;
RX MEDLINE=22692404; PubMed=12807452;
RA Leterrier C., Perelle S., Dillasser F., Fach P.;
RT "Identification of a new putative enterotoxin seu encoded by the egc
RT cluster of Staphylococcus aureus."
RT J. Appl. Microbiol. 95:38-43(2003).
DR EMBL; AY205305; AAP41901.1; -;
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
```


RC STRAIN-AS14;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RA Villani F.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291445; AAP78526.1; -
DR HSSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogenes; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 218
FT SEQUENCE 218 AA; 24993 MW; 6988BCE49754350 CRC64;

Query Match 23.2%; Score 287.5; DB 2; Length 218;
Best Local Similarity 34.0%; Pred. No. 1,1e-15;
Matches 70; Conservative 34; Mismatches 69; Indels 33; Gaps 7;

QY 23 LSNLRQIY---YNEKAITENKESDDQPLENTLLFKGFFTHPMYNDLLVDLGSKDQTN 78
DB 30 VGNLRFYTKHDYIDLKGVTDKPLPIANQLE-----FSTG---TNDLISSNNWDEIS 79
QY 79 KYKGGKVDLYGAYVYQACAGTPNTACMYGVTLDHNNRLTEKKVPINIMIDGKQTV 138
DB 80 KKGKKLIDIFGIDYNGPC-----KSKYWGATL-SCGYLSARKIPINLWNGKHKT 132
QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFG-GK-----VQGLIVF 186
DB 133 STDKATNKLVTAGIDVLRKYIQLQEEVNIYGHNTGKGEYKSKFYSGFNNKVL 192
QY 187 HSESGTWSYDLPDAGQGYPTLLRI 212
DB 193 HLNNEKSFSDLPYTGDLPSVFLKI 218

RESULT 68
Q7X0E9 PRELIMINARY; PRT; 218 AA.
AC Q7X0E9;
DT 01-OCT-2003 (T-EMBLrel. 25, Last Created)
DT 01-OCT-2004 (T-EMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
DE Enterotoxin type I (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RI;
RA Blaiotta G., Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RA Villani F.;
RL Submitted (MAY-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291443; AAP78522.1; -
DR HSSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogenes; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 218
FT SEQUENCE 218 AA; 24994 MW; 698329CE49754350 CRC64;

Query Match 23.1%; Score 286.5; DB 2; Length 218;
Best Local Similarity 34.0%; Pred. No. 1,4e-15;
Matches 70; Conservative 34; Mismatches 69; Indels 33; Gaps 7;

QY 23 LSNLRQIY---YNEKAITENKESDDQPLENTLLFKGFFTHPMYNDLLVDLGSKDQTN 78

DB 30 VGNLRFYTKHDYIDLKGVTDKPLPIANQLE-----FSTG---TNDLISSNNWDEIS 79
QY 79 KYKGGKVDLYGAYVYQACAGTPNTACMYGVTLDHNNRLTEKKVPINIMIDGKQTV 138
DB 80 KKGKKLIDIFGIDYNGPC-----KSKYWGATL-SCGYLSARKIPINLWNGKHKT 132
QY 139 PIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFG-GK-----VQGLIVF 186
DB 133 STDKATNKLVTAGIDVLRKYIQLQEEVNIYGHNTGKGEYKSKFYSGFNNKVL 192
QY 187 HSESGTWSYDLPDAGQGYPTLLRI 212
DB 193 HLNNEKSFSDLPYTGDLPSVFLKI 218

RESULT 69
Q06531 PRELIMINARY; PRT; 239 AA.
AC Q06531;
DT 01-NOV-1996 (T-EMBLrel. 01, Last Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (T-EMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9401133; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
biological and evolutionary implications";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; L13374; AAA26518.1; -
DR HSSP; P23313; 1KLD.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pachogenes; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactL_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1
FT SEQUENCE 239 AA; 27612 MW; BB7BD6204731ED24 CRC64;

Query Match 23.1%; Score 285.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 1,8e-15;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLAKSELEQNALSNLRQIYYNEKAITENK-ESDDQPLENTLLFKGFFTHPMYNDLLV 69
DB 10 DLKSSSP-TGTGNMNM--LYIDHYVSATKVSVDKFLAHDIYINISDGLKNYDVKT 66
QY 70 DLGSKDNTKRYKAKKVDLYGAYVYQAC-----AGTPNTACMYGVTLDHNNRLTEE 122
DB 67 ELINEDLAKKYKQVVDVGSNNYVNCYFSSKDNVGVGTGCMYGGITKHGNNHNDG 126
QY 123 --KKVPINIMIDGKQTVPIDKVTSKKEVTVQELDLQARHYLHGKGLYNSDSFGKQV 180
DB 127 NLQNVLVRYV-ENKRYTISFE-VQTDKSVTAQELIKANFLINKNLYEENS--SPYE 182
QY 181 RGLIVHSESGTWSYDLPDAGQGYPT--TLRIYRDNKTINSENLHIDLYLT 232
DB 183 TGIIFLENNGNFTWDMFAPDQKFDQSKYILMTNDKNTVDSKSKYIVHLTT 236

RESULT 70

```

Q06532      PRELIMINARY; PRT; 239 AA.
AC Q06532;
DT 01-NOV-1996 (TREMBLrel. 01. Created)
DT 01-NOV-1996 (TREMBLrel. 01. Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25. Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBITaxID=1280;
[1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; I13375; AAA26619.1; -.
DR HSP; P23313; IKLU.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C.1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 239 AA; 27642 MW; C77009F46BC8D645 CRC64;

Query Match 23.1%; Score 285.5; DB 2; Length 239;
Best Local Similarity 32.1%; Pred. No. 18e-15;
Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

QY 11 DLRRKSELQRNALSLRQIYYNEKATENK-ESDDQELNTLRFKGFTHPMYNDLLV 69
DB 10 DLHSSSE-TEGMDMK--VLYDDHYGATKYKSDKFLAHLIYNISDKLAKNDKXT 66
QY 70 DLGSKDATNKKKKKVDLYGAYYQC-----AGTPNKTCMYGVTLHDNNRLTEE 122
DB 67 ELLMEDLAKKYYDEVVDYGSNYNVCYFSSKDNVGYGKTCMYGGITKEGHPDNG 126
QY 123 --KKVPINLMDGKQTTPIDKVTSKKEVYQGEIDLAQAHYHAKRFGLYNDSFGKQV 180
DB 127 NLQNVLVVY-BNKKNTISFE-VQTDKKSVTAGQBLDIKARNFLINKKQLYEPNS--SPYE 182
QY 181 RGLVFSSEGSSTVYDFDAQGGYPD--TLRIYRDNKNTINSENIHIDLYLT 232
DB 183 TGYIKFIENNNTFWYDMMPARGDKFDQSKYLMWNNDKTKVDSKVKLEVHLTT 236

RESULT 71
ETC3 STAM STANDARD; PRT; 266 AA.
AC P23313;
DT 01-NOV-1991 (Rel. 20. Created)
DT 01-NOV-1991 (Rel. 20. Last sequence update)
DT 25-OCT-2004 (Rel. 45. Last annotation update)
DE Enterotoxin type C-3 precursor (SEC3).
GN Name=entC3; OrderedLocNames=SAV2009, SA1817;
OS Staphylococcus aureus (strain Mu50 / ATCC 700699).
OS Staphylococcus aureus (strain N315), and
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
NC NCBITaxID=158878, 158879, 1280;
[1]
RP SEQUENCE FROM N.A.
RX STRAIN=Mu50 / ATCC 700699, and N315;
RX MEDLINE=21311952; PubMed=11418146; DOI=10.1016/S0140-6736(00)04403-2;

```

```

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,
RA Kamori M., Matsumaru H., Maruyama A., Murakami H., Hoshiyama A.,
RA Mizutani-Ui Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaito C.,
RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,
RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,
RA Hatori M., Ogasawara N., Hayashi H., Hiratsuki K.;
RT "Whole genome sequencing of methicillin-resistant Staphylococcus
RT aureus.";
RL Lancet 357:1225-1240(2001).
[2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90220508; PubMed=2235627;
RA Hovde C.U., Hackett S.P., Bohach G.A.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C3 gene:
RT sequence comparison of all three type C staphylococcal enterotoxins.";
RL Mol. Gen. Genet. 220:329-333(1990).
[3]
RP X-RAY CRYSTALLOGRAPHY (3.5 ANGSTROMS) OF COMPLEX WITH TCR.
RX MEDLINE=97064178; PubMed=8906797; DOI=10.1038/384188a0;
RA Fields B.A., Malchiodi E.L., Li H., Ysern X., Stauffacher C.V.,
RA Schlievert P.M., Karjalainen K., Mariuzza R.A.;
RT "Crystal structure of a T-cell receptor beta-chain complexed with a
RT Nature 384:188-192(1996).
RL Nature 384:188-192(1996).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; AP003364; BAB58171.1; -.
DR EMBL; AP003135; BAB43097.1; -.
DR EMBL; X51661; CAA35972.1; -.
DR PIR; S11885; S11885.
DR PDB; 1JCK; X-ray; B/D=28-266.
DR PDB; 1JMM; X-ray; D=28-266.
DR PDB; 1JWS; X-ray; D=28-266.
DR PDB; 1JWU; X-ray; D=28-266.
DR PDB; 1KLU; X-ray; D=28-266.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF02876; Staph_tox_C.1.
DR Pfam; PF01123; Staph_tox_OB.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW 3D-structure; Complete proteome; Enterotoxin; Signal; Superantigen;
KW Toxin.
FT SIGNAL 1 27
FT CHAIN 28 266 Enterotoxin type C-3.
FT DISULFID 120 137
FT HELIX 35 37
FT HELIX 41 43
FT STRAND 44 44
FT STRAND 48 48
FT TURN 49 49
FT HELIX 49 55
FT STRAND 60 65
FT STRAND 69 69

```

```

FT TURN 73 74
FT STRAND 75 79
FT TURN 83 85
FT STRAND 90 94
FT HELIX 98 105
FT TURN 106 106
FT STRAND 109 113
FT STRAND 116 116
FT TURN 118 119
FT STRAND 135 139
FT STRAND 142 144
FT TURN 146 147
FT STRAND 149 149
FT TURN 151 153
FT STRAND 156 164
FT TURN 165 166
FT STRAND 167 176
FT STRAND 178 178
FT STRAND 180 182
FT HELIX 183 198
FT STRAND 210 216
FT TURN 218 219
FT STRAND 222 226
FT STRAND 232 232
FT STRAND 237 241
FT HELIX 242 246
FT STRAND 249 251
FT TURN 252 254
FT STRAND 256 262
SQ SEQUENCE 266 AA; 30671 MW; 5ED8A32D11FCA59 CRC64;

```

Query Match 23.1%; Score 285.5; DB 1; Length 266;
 Best Local Similarity 32.1%; Pred. No. 2.1e-15;
 Matches 75; Conservative 49; Mismatches 91; Indels 19; Gaps 9;

```

QY 11 DLKKSELRNALSNLRQIYYNEKAITENK-ESDDQPLENTLFPKGFTGHPWYNDLLV 69
DB 37 DLKSESEF-TGTMGNMK--YLDDHYVSATKYSVDKFLAHLDIYINHKKLNNYDKVKT 93
QY 70 DLGSKDATNKYKGVLDYGYAYGYQC-----AGTPTNKTCMYGVTGLHDNNRLTEE 122
DB 94 ELINEDLAKNYDEVDVYGSNYVNCYFSSKDNVGVKTGKTCMYGGITKHEGNHFDNG 153
QY 123 --KYPINIMIDGKQTVTVIDKVTSKKEVTVOELDLOARHYLHGFGLYNSDSFGKQVQ 180
DB 154 NLQNVILIRYV-ENKRWTSIFE-VQTDKSVTAQELDIKANKFLINKNLYERNFNS--SPYE 209
QY 181 RGLIVHSESGSTVSYDLFDAQGYPD--TLRIYRDNKNTINSENLHIDLVTYT 232
DB 210 TGYIKETENNNGTFTWDMMPAPGDKFDQSKYLMITNDKNTVDSKSYKIEVHLTT 263

```

RESULT 72
 006535 PRELIMINARY; PRT; 239 AA.
 AC 006535;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
 DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
 DE Enterotoxin (Fragment).
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 OX (1)
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94011313; PubMed=8406814;
 RA Marr J.C., Lyon J.D., Roberson J.R., Lupher M., Bohach G.A.;
 RT "Characterization of novel type C staphylococcal enterotoxins:
 biological and evolutionary implications."
 RL Infect. Immun. 61:4254-4262(1993).
 DR EMBL; L13377; AAA26621.1; -.
 DR PDB; 1CKI; X-ray; A=1-239.
 DR GO; GO:0005576; C:extracellular; IEA.

```

DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin_1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27648 MW; CC3CB3B04E4119E0 CRC64;

```

Query Match 23.0%; Score 284.5; DB 2; Length 239;
 Best Local Similarity 32.5%; Pred. No. 2.2e-15;
 Matches 76; Conservative 48; Mismatches 91; Indels 19; Gaps 9;

```

QY 11 DLKKSELRNALSNLRQIYYNEKAITENK-ESDDQPLENTLFPKGFTGHPWYNDLLV 69
DB 10 DLKSESEF-TGTMGNMK--YLDDHYVSATKYSVDKFLAHLDIYINHKKLNNYDKVKT 66
QY 70 DLGSKDATNKYKGVLDYGYAYGYQC-----AGTPTNKTCMYGVTGLHDNNRLTEE 122
DB 67 ELINEDLAKNYDEVDVYGSNYVNCYFSSKDNVGVKTGKTCMYGGITKHEGNHFDNG 126
QY 123 --KYPINIMIDGKQTVTVIDKVTSKKEVTVOELDLOARHYLHGFGLYNSDSFGKQVQ 180
DB 127 NLQNVILIRYV-ENKRWTSIFE-VQTDKSVTAQELDIKANKFLINKNLYERNFNS--SPYE 182
QY 181 RGLIVHSESGSTVSYDLFDAQGYPD--TLRIYRDNKNTINSENLHIDLVTYT 232
DB 183 TGYIKETENNNGTFTWDMMPAPGDKFDQSKYLMITNDKNTVDSKSYKIEVHLTT 236

```

```

QY 005157 PRELIMINARY; PRT; 239 AA.
DB 005157;
DT 01-JUL-1997 (TEMBLrel. 04, Created)
DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Type C enterotoxin (Fragment).
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1285;
OX (1)
RP SEQUENCE FROM N.A.
RC STRAIN=95-011195;
RA Edwards V.M., Deringer J.R., Gallantine S.D., Deobald C.F.,
  Berger P.H., Kaput V., Stauffacher C.V., Bohach G.A.;
  Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RL EMBL; U91526; AAB50248.1; -.
DR HSSP; P23313; 1UWM.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_toxin_1.
DR Pfam; PF02876; Staph_tox_C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27536 MW; D6606446600E4191 CRC64;

```

Query Match 22.9%; Score 283.5; DB 2; Length 239;
 Best Local Similarity 33.5%; Pred. No. 2.7e-15;
 Matches 79; Conservative 44; Mismatches 90; Indels 23; Gaps 10;

```
QY 11 DLRRKSELQARNALSNLROIY--YNEKAITENK-ESDDQFLENTLLFKGFPTGHPWINDL 67
DB 10 DLHKSSEF-TGTMGMMKCLYDDY---VSATKVSVPKFLAHLIDLYINISPKLKNYDKV 64
QY 68 LVLDGSDATNKYKGVKVDLYGAYYGQC-----AGGTPNKTAQWYGLTHDNHNLTL 120
DB 65 KTELINEDLAKKYKQVDEVDVGSNYYNVCYSSKDNVKGKVTGKTCMGGLTKHEGNHFD 124
QY 121 EE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHGKFGLYNSDPSFGK 178
DB 125 NGNQNVLIRIY-ENKNTISFD-VQTDKSVTAQELDIKARNFLINKNLYEENS--SP 180
QY 179 VQRGILVHSESGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLYLT 232
DB 181 YETGYIKFIESNDNTPWYDMMPAPGDKFDQSKYLMYISDNKTVDKSKVIEVHLTT 236

RESULT 74
Q8NXJ6 PRELIMINARY; PRT; 266 AA.
AC Q8NXJ6;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE ENTEROTOXIN type C.
GN Name=sec4; OrderedLocuNames=MW0759;
OS Staphylococcus aureus (strain MW2).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=196620;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MW2;
RX MEDLINE=2040717; PubMed=12044378; DOI=10.1016/S0140-6736(02)08713-5;
RA Baba T., Takeuchi F., Kuroda H., Yuzawa H., Aoki K.-I., Oguchi A.,
RA Nagai Y., Iwama N., Asano K., Naito T., Kuroda H., Cui L.,
RA Yamamoto K., Hirumatsu K.,
RT "Genome and virulence determinants of high virulence community-
RT acquired MRSA."
RL Lancet 359:1819-1827(2002).
DR EMBL; AP004824; BAB94624.1; -.
DR HSSP; P34071; 1STE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Complete proteome.
SQ SEQUENCE 266 AA; 30670 MW; 4C654659AA48120F CRC64;

Query Match 22.9%; Score 283.5; DB 2; Length 266;
Best Local Similarity 31.1%; Pred. No. 3.1e-15;
Matches 76; Conservative 50; Mismatches 99; Indels 19; Gaps 9;

QY 1 SEKSEINEKDLRKSELOARNALSNLROIYYNEKAITENK-ESDDQFLENTLLFKGFPT 59
DB 27 AESQDPPTPDEIHKSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHLIDLYINISDK 83
QY 60 GHPWYNDLLVLDGSDATNKYKGVKVDLYGAYYGQC-----AGGTPNKTAQWYGLVT 112
DB 84 KLKNYDKVKTLEINEDLAKKYKQVDEVDVGSNYYNVCYSSKDNVKGKVTGKTCMGGLT 143
QY 113 LHDNNRLTEE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHGKFGLY 170
DB 144 KHEGNHFNPNGLNQNVLIRIY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLY 201
QY 171 NSDSFGKQVRGLIVHSESGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDL 228
```

```
DB 202 EFNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLMYINDNKTVDKSKVIEV 259
QY 229 YLYT 232
DB 260 HLTT 263

RESULT 75
Q06533 PRELIMINARY; PRT; 239 AA.
AC Q06533;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Enterotoxin (fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=9401313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications."
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13378; AAA26622.1; -.
DR HSSP; P34071; 1STE.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON TER 1
SQ SEQUENCE 239 AA; 27651 MW; A21A954386A8E8625 CRC64;

Query Match 22.8%; Score 282.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 3.3e-15;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELOARNALSNLROIYYNEKAITENK-ESDDQFLENTLLFKGFPTG 60
DB 1 ESQDPPTPDEIHKSEF-TGTMGNMK--YLYDDHYVSATKVSVDKFLAHLIDLYINISPK 57
QY 61 HPWYNDLLVLDGSDATNKYKGVKVDLYGAYYGQC-----AGGTPNKTAQWYGLT 113
DB 58 LKNYDKVKTLEINEDLAKKYKQVDEVDVGSNYYNVCYSSKDNVKGKVTGKTCMGGLTK 117
QY 114 HDNNRLTEE--KKVPINIMIDGKQTTVPIDKYKTSKEVTVQELDLQARHYLHGKFGLY 171
DB 118 HEGNHFNPNGLNQNVLIRIY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
QY 172 SDSFGKQVRGLIVHSESGSTVSYDLFDAQGYPD--TLRIYRDNKTINSENHLIDLY 229
DB 176 FNS--SPYETGYIKFIENNNGNTFWYDMMPAPGDKFDQSKYLMYINDNKTVDKSKVIEV 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 76
ETC2_STAU STANDARD; PRT; 266 AA.
ID ETC2_STAU
AC P34071;
DT 01-FEB-1994 (Rel. 28, Created)
```

DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Enterotoxin type C-2 precursor (SEC2).
 GN Name=entC2;
 OS Staphylococcus aureus.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
 OX NCBI_TaxId=1280;
 RN
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 28-66.
 RX MEDLINE=89277549; PubMed=2543637;
 RA Bohach G.A., Schlievert P.M.;
 RT "Conservation of the biologically active portions of staphylococcal enterotoxins C1 and C2".
 RL Infect. Immun. 57:2249-2252(1989).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RX MEDLINE=96027099; PubMed=7582894; DOI=10.1016/S0969-2126(01)00212-X;
 RA Papageorgiou A.C., Acharya K.R., Shapiro R., Passalacqua B.F.,
 RA Brehm R.D., Tranter H.S.;
 RT "Crystal structure of the superantigen enterotoxin C2 from Staphylococcus aureus reveals a zinc-binding site".
 RL Structure 3:769-779(1995).
 RN
 RP X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS).
 RX MEDLINE=96022987; PubMed=7552730;
 RA Swaminathan S., Furey W.R. Jr., Fletcher J., Sax M.;
 RT "Residues defining V beta specificity in staphylococcal enterotoxins".
 RL Nat. Struct. Biol. 2:680-686(1995).
 RN
 RP COMPARISON OF STRUCTURE OF SEA AND SEC2.
 RX MEDLINE=9734373; PubMed=9191070; DOI=10.1006/jmbi.1997.1023;
 RA Schad E.M., Papageorgiou A.C., Svensson L.A., Acharya K.R.;
 RT "A structural and functional comparison of staphylococcal enterotoxins A and C2 reveals remarkable similarity and dissimilarity".
 RL J. Mol. Biol. 269:270-280(1997).
 CC
 RT -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication staphylococcal food poisoning syndrome. The illness characterized by high fever, hypotension, diarrhea, shock, and in some cases death.
 CC
 RT -1- COFACTOR: Binds 1 zinc ion per subunit. The zinc ion is necessary for the toxin interaction with MHC class II.
 CC
 RT -1- SUBCELLULAR LOCATION: Secreted.
 CC
 RT -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin family.
 CC
 PIR: A60114; A60114.
 DR PDB: 1COV; X-ray; A=28-266.
 DR PDB: 1I4P; X-ray; A=28-266.
 DR PDB: 1I4Q; X-ray; A=28-266.
 DR PDB: 1I4R; X-ray; A=28-266.
 DR PDB: 1I4X; X-ray; A=28-266.
 DR PDB: 1SE2; X-ray; @=28-266.
 DR PDB: 1STE; X-ray; @=28-266.
 DR PDB: 1UNS; X-ray; A=28-266.
 DR InterPro: IPR008992; Bact_endotox.
 DR InterPro: IPR006177; Bactl_tox.
 DR InterPro: IPR006123; Staph/Strep_toxin.
 DR InterPro: IPR006126; Staph/Strep_tox.
 DR InterPro: IPR006173; Staph_tox_OB.
 DR Pfam: PF02876; Staph_Strep_tox_C1.
 DR Pfam: PF01123; Staph_Strep_toxin; 1.
 DR PRINTS: PR00279; BACTRLTOXIN.
 DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
 DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
 KW 3D-structure: Direct protein sequencing; Enterotoxin; Metal-binding; Signal; Superantigen; Toxin; Zinc.
 KM
 FT SIGNAL 1 27
 FT CHAIN 28 266 Enterotoxin type C-2.
 FT DISULFID 120 137
 FT METAL 36 36 Zinc.
 FT METAL 110 110 Zinc.
 FT METAL 145 145 Zinc.
 FT METAL 149 149 Zinc.

FT HELIX 35 37
 FT HELIX 41 43
 FT STRAND 44 44
 FT TURN 48 48
 FT TURN 49 49
 FT STRAND 50 55
 FT STRAND 59 65
 FT STRAND 69 69
 FT TURN 73 74
 FT STRAND 75 79
 FT TURN 83 86
 FT STRAND 90 94
 FT HELIX 98 104
 FT TURN 105 106
 FT STRAND 109 113
 FT STRAND 116 116
 FT TURN 118 119
 FT TURN 128 129
 FT STRAND 136 139
 FT STRAND 142 144
 FT TURN 146 147
 FT STRAND 149 149
 FT HELIX 151 153
 FT STRAND 156 164
 FT TURN 165 166
 FT STRAND 167 176
 FT STRAND 178 178
 FT STRAND 180 182
 FT HELIX 183 198
 FT STRAND 208 216
 FT TURN 218 219
 FT STRAND 222 226
 FT STRAND 232 232
 FT HELIX 237 241
 FT HELIX 242 246
 FT STRAND 249 251
 FT TURN 252 254
 FT TURN 256 263
 SQ SEQUENCE 266 AA; 30604 MW; 8407FB18536FAC08 CRC64;
 Query Match 22.7%; Score 281.5; DB 1; Length 266;
 Best local Similarity 31.1%; Pred. No. 4,5e-15;
 Matches 76; Conservative 50; Mismatches 99; Indels 19; Gaps 9;
 QY 1 SEKSEINERKDKPKSELQRMNLNROLYYVNEKAITENK-ESDDQPLENTLLPFGKFT 59
 DB 27 AESQPDPTDELRKSSRP-TGTWGNK--YLYDDHYVASATKWSVDKFLAHLILINISDK 83
 QY 60 GHPWYNDLVDLSKDATNKKKGYDLGAYYGYOC-----AGTPNKTKAMYGVT 112
 DB 84 KLMYKVKTELLNELAKKIDVVDYGSNTYVNCYSSKDNKVGKVGKTCMGGIT 143
 QY 113 LHDNNRLTEB--KVPINIMIDKQTPVPIDKYTSKEVTVOELDQARHYLHGKFLY 170
 DB 144 KHEGNHFDNGNLDQNLIRVY-ENKRNITISPE-VQTDKKSVAQELDIKANPFIINKNLY 201
 QY 171 NSPSFGKVGKGLIVHSSSGSVSYDLPDAGQYD--TLLEIYDNNKINSENLHIDL 228
 DB 202 EFNSS--SPYETGIKIEINNGNTFWYDMPAPDQKFDQSRYLMMYDNNKTVDSKSVKIEV 259
 QY 229 YLYT 232
 DB 260 HLTT 263
 RESULT 77
 07X0E6 PRELIMINARY; PRT; 207 AA.
 AC 07X0E6;
 DT 01-OCT-2003 (TRMBLrel. 25, Created)
 DT 01-OCT-2003 (TRMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Enterotoxin type I (Fragment).
 OS Staphylococcus aureus.

```
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BS69;
RA Blotica G.; Pennacchia C., Casaburi A., Ercolini D., Fusco V.,
RL Villani F.;
RL Submitted (May-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY291446; AAP78528.1; -.
DR HSSP; P13163; IESF.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_cox_C_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 207
SQ SEQUENCE 207 AA; 23867 MW; C815DEC021FPA681 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 207;
Best Local Similarity 34.7%; Pred. No. 4e-15;
Matches 67; Conservative 32; Mismatches 61; Indels 33; Gaps 7;

QY 23 LSNLRQIY-----YNEKAITENKESDDQFLENTLLFKGFPTGHPWYNDLVLDGSKDXTN 78
DB 30 VGNLRNFYTKHDYIDLKGVTDKNLPIANQLF-----FSTG---TNDLISESNWDEIS 79
QY 79 KYGKKVDLYGAYGYQCAGTGNKTAQMGVTVLHDNNRLTEKKVPIINLMIDKQTTV 138
DB 80 KFKGKDDIFGIDVNGPC-----KSKYMGATL-SCQYNSARKIPINLMVNGKHKT 132
QY 139 PIDKVTSSKEVTVQVELDQARHYLHGKFGLYNSDSFG-GK-----VGRLIVF 186
DB 133 STDKAIATKKVLTVAQELVTKLRVYLOEENYVGHNNYTGKGYKSKFYSGFNNKVLV 192
QY 187 HSSGSGTVSYDLF 199
DB 193 HLNNEKSPSYDLF 205

RESULT 78
Q6XZB6 PRELIMINARY; PRT; 222 AA.
AC Q6XZB6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Enterotoxin seb variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=339E;
RL MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RA Lerecette C., Perelle S., Dilaeser F., Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
RT genes sea to sea of Staphylococcus aureus.";
RL Mol. Cell. Probes 17:227-235(2003).
DR EMBL; AY196689; AAP37186.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_cox_C_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
```

```
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 26355 MW; E699C4F9BA858D50 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 222;
Best Local Similarity 34.5%; Pred. No. 4.4e-15;
Matches 78; Conservative 42; Mismatches 87; Indels 19; Gaps 8;

QY 11 DLRRKSELQRNALNLRQIYNYNEKAITENKESDDQFLENTLLFKGFPTGHPWYNDLVLD 70
DB 2 ELHRSKR-TGLMNMKVLVDNHSVAI-NVKSIDQFLYPLILISYIKTKGANDNVAVE 59
QY 71 LGSKDANIKYKKVVDLYGAYGYQC-----AGTPNKTAQMGVTVLHDNNRLT 120
DB 60 FKNIDLDKVDKQYVDGAYGYQCPSKKTNDINSHQTKRKYCMYGGVTEHNGQLD 119
QY 121 EEKVPIINLMIDGQTTVPIDKVTSSKEVTVQVELDQARHYLHGKFGLYNSDSFGKVLQ 180
DB 120 KYRSITVAVFEDGK-NLISFD-VQTNKKVTAQELDYLTRHYLVNKKLYEFNN--SPYE 175
QY 181 RGLIVFHSSGSGTVSYDLFDAQGYPD--TLRIYRDNKNTINSENL 224
DB 176 TGYIKTFISENS-FWYDMFAPGDKFDQSKYLMYTNNDKLVDSKDV 220

RESULT 79
Q6ST49 PRELIMINARY; PRT; 239 AA.
AC Q6ST49;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin C2 (Fragment).
GN Name=SEC2;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RA Xu M., Zhang C.;
RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY450554; AAR20496.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; BactI_cox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph_cox_OB.
DR Pfam; PF01123; Staph_strep_toxin_1.
DR Pfam; PF02876; Staph_strep_cox_C_1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT CHAIN 1
SQ SEQUENCE 239 AA; 27585 MW; 6A7828027F893822 CRC64;

Query Match 22.7%; Score 280.5; DB 2; Length 239;
Best Local Similarity 31.3%; Pred. No. 4.8e-15;
Matches 76; Conservative 49; Mismatches 99; Indels 19; Gaps 9;

QY 2 EKSEINEKDLRKSELRNALNLRQIYNYNEKAITENK-ESDDQFLENTLLFKGFPTG 60
DB 1 ESQDPPTPEDELHKSSSF-TGTMGNMK--LYVDHIVSATKVMVDKFLAHLIINISDK 57
QY 61 HPWYNDLVLDGSKDANIKYKKVVDLYGAYGYQC-----AGTPNKTAQMGVTVL 113
DB 58 LKVDKVTTELNDLAKKYDEVVDVGSNYVNCYSSKDNVGVKTVGKTCMGVGTIK 117
QY 114 HDNNRLTEE--KKVPIINLMIDGQTTVPIDKVTSSKEVTVQVELDQARHYLHGKFGLYN 171
```

```
Db 118 HEGNHFDNGNLQNVILIRY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLYE 175
Qy 172 SPSFGKQVGRGLIVHSSGSGTVSYDLFDAQGYPD--TLIRYRNKNTINSENHLIDY 229
Db 176 FNS--SPYETGYIKFIENNNGNTFWYDMPADGDKFQSKYLMYNDKNTVDSKXIEVH 233
Qy 230 LYT 232
Db 234 LTT 236

RESULT 80
054696 PRELIMINARY; PRT; 236 AA.
ID 054696;
AC 054696;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=spea;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Selaender R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes."
RL J. Exp. Med. 174:1271-1274 (1991).
DR EMBL; X61573; CAA43771.1; -.
DR PIR; S18789; S18789.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strip_toxin; 1.
DR Pfam; PF02876; Staph_Strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KM Signal
FT NON_TER 1 1
FT SIGNAL <1 22 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27575 MW; 70F54120E79127DF CRC64;

Query Match 22.6%; Score 279.5; DB 2; Length 236;
Best Local Similarity 33.5%; Pred. No. 5.7e-15;
Matches 76; Conservative 4; Mismatches 99; Indels 11; Gaps 7;

Qy 4 SEINKEKDLRKSELDQNAL-SNLRQY--YNEKATEKESDDQPLENTLLFKGFTG 60
Db 17 SGEVFAQODBNPESQLHRSSLVKNLQNTFLYEGDPVAVHENVKVDLSHDLIN--VS 73
Qy 61 HPWYNDLVDLGSKDATNKYKGVLDYGAAYGYOC-AGSTPNKTAQMGYVTLHDNRL 119
Db 74 GLNYVDLKTETLKNREKSTLFGKNQVDIYGVYYHYCYLGNNAKRRACIYGGVTHNENHL 133
Qy 120 TEKKKYPINIMIGKQTTVPIDKYKTSKKEVTVQEDLQARHYLHGKFGLYNSDSFGKY 179
Db 134 EIRKNLILVAKYSIGIQ-SLSFD-IEFSKQNTAQEILDYKVRKHLTDKQLYTNGP--SKY 189
Qy 180 QRGILYFHSSEGSVSYDLFDAQGYPDTLIRYRNKNTINSENHL 226
```

```
Db 190 ETGYIKFISKDETFWDFEPPEPFNQVKYLMYXNDNETLDSSTSQI 236
RESULT 81
09F0L6 PRELIMINARY; PRT; 271 AA.
ID 09F0L6;
AC 09F0L6;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Staphylococcal enterotoxin C-bovine.
GN Name=sec-bov;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_Taxid=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20566668; PubMed=11114901; DOI=10.1128/JB.183.1.63-70.2001;
RA Fitzgerald J.R., Monday S.R., Foster T.J., Bohach G.A., Hartigan P.J.,
RA Meaney W.J., Smyth C.J.;
RT "Characterization of a putative pathogenicity island from bovine
RT Staphylococcus aureus encoding multiple superantigens."
RL J. Bacteriol. 183:63-70 (2001).
DR EMBL; AF217235; AAG29599.1; -.
DR HSSP; P34071; I14X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bcrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_Strip_toxin; 1.
DR Pfam; PF02876; Staph_Strip_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 271 AA; 31267 MW; 3493F6228B042F10 CRC64;

Query Match 22.6%; Score 279.5; DB 2; Length 271;
Best Local Similarity 30.7%; Pred. No. 6.7e-15;
Matches 75; Conservative 53; Mismatches 97; Indels 19; Gaps 9;

Qy 1 SEKSEINKEKDLRKSELDQNAL-SNLRQY--YNEKATEKESDDQPLENTLLFKGFT 59
Db 32 ASQDPPTDELDHAKSKF-TGLMKNKVL--YDGRVSAIKVKSVDKFLAHLIDINISDK 88
Qy 60 GHPWYNDLVDLGSKDATNKYKGVLDYGAAYGYOC-----AGSTPNKTAQMGYV 112
Db 89 KLNKYKVTETLNEBLAKKYDEVDYGSNYYVNCYSSKQNVKVGKTCMGIT 148
Qy 113 LHDNNRLTEBK--KVPINIMIGKQTTVPIDKYKTSKKEVTVQEDLQARHYLHGKFG 170
Db 149 KHGHNHFDNGNLQNVILIRY-ENKNTISFE-VQTDKSVTAQELDIKARNFLINKNLY 206
Qy 171 NSDSFGKQVGRGLIVHSSGSGTVSYDLFDAQGYPD--TLIRYRNKNTINSENHL 228
Db 207 EFNS--SPYETGYIKFIENNNGNTFWYDMPADGDKFQSKYLMYNDKNTVDSKXIEV 264

Qy 229 LYT 232
Db 265 LTT 268

RESULT 82
P97163 PRELIMINARY; PRT; 236 AA.
ID P97163;
AC P97163;
DT 01-MAY-1997 (TrEMBLrel. 03, Created)
DT 01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Type A exotoxin precursor (Fragment).
GN Name=spea;
```

```
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS165, MGAS327, MGAS493, MGAS494, MGAS167, and MGAS156;
RC MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlivert P.M., Seldner R.K., Musser J.M.;
RA "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61556; CAA43754.1; -.
DR EMBL; X61555; CAA43753.1; -.
DR EMBL; X61557; CAA43755.1; -.
DR EMBL; X61558; CAA43756.1; -.
DR EMBL; X61559; CAA43757.1; -.
DR EMBL; X61560; CAA43758.1; -.
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR Signal.
KW NON_TER
FT SIGNAL 1 1 Potential.
FT CHAIN 23 >236 type A exotoxin.
FT NON_TER 236 236
SQ SEQUENCE 236 AA; 27454 MW; 3FB3F41ABDC13A84 CRC64;

Query Match 22.5%; Score 278.5; DB 2; Length 236;
Best Local Similarity 33.8%; Pred. No. 6e-15;
Matches 78; Conservative 43; Mismatches 91; Indels 19; Gaps 10;

OY 4 SEINEKDLRKSELORNAL-SNLROIYY-YNEKAIT-ENKESDDQFLNTLLFKGPFPG 60
DB 17 SQEVAQODPPDSQLHRSLSLVKLNQNIYFLYEGDPVTHENVASVQQLSHDLIYN---VS 73
OY 61 HPWYNDLLVDLGSKDATNKKYKGVLDYGAYYGYOC-AGGTENKTAQMTGYTLHDNNRL 119
DB 74 GPNYDKLKTLELNQEMATLFDKNDVIYGEVYHLCYLENABRSACIYGVTHNHEGNHL 133
OY 120 TEKKVPIINLMTDQGTVPIDKVTSKKEVVOELDLARHYLHGKFGFLVNSDSFGGKV 179
DB 134 EIPKRIIVKVSIDGQ-SLSPD-IEFNKKMVAQELDYVRRYLLTDNKQLYNNGP-SKY 189
OY 180 QRGILVFSSEGSTVSVDLFD---AQCQYPTLLRIYDNKNTINSENHII 226
DB 190 ETGYIKFIPKNSEFWFDFPPEPFTQSKY----LMIYDNNTLDSNISI 236

RESULT 83
O53678 PRELIMINARY; PRT; 239 AA.
ID O53678;
AC O53678;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Streptococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCB1_TaxID=1280;
RN [1]
```

```
RP SEQUENCE FROM N.A.
RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Luper M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13376; AAA26620.1; -.
DR HSSP; P34071; 1I4X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bact_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin_1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTR_TOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
DR NON_TER 1 1
SQ SEQUENCE 239 AA; 27618 MW; A13E7EB25C6989C2 CRC64;

Query Match 22.5%; Score 278.5; DB 2; Length 239;
Best Local Similarity 30.9%; Pred. No. 7e-15;
Matches 75; Conservative 52; Mismatches 97; Indels 19; Gaps 9;

OY 2 EKSEINEKDLRKSELORNAL-SNLROIYYNEKAITENK-ESDDQFLNTLLFKGPFPG 60
DB 1 ESQPPPTDELHKASKF-TGLMENKVL--YDRVVSATKYSVDKFLAHLIIVNISDK 57
OY 61 HPWYNDLLVDLGSKDATNKKYKGVLDYGAYYGYOC-----AGGTENKTAQMTGYTL 113
DB 58 LKNYDKVKTLELNEDLAKKYDEVVDYGSNYYNVCYSSKDNQKVTGKTQMTGYTLK 117
OY 114 HDNRRLTEEK--KVPINIMIDGKQTVPIIDKVTSKKEVVOELDLARHYLHGKFGFLN 171
DB 118 HEGNHFNDGKIQNVILIRY-ENKRTISFE-VQDDKSVTAQELDKARNFLINKNLIYE 175
OY 172 SDSFGKVGQGLIVFSSEGSTVSVDLFDPAQGYPD--TLRIYDNKNTINSENHIDLY 229
DB 176 FNS--SPETGYIKFIENKNGTFTWDMIPAQDKFDQSKYLMYNDKNTIVSKSVKIVH 233
OY 230 LYT 232
DB 234 LTT 236

RESULT 84
O938P4 PRELIMINARY; PRT; 222 AA.
ID O938P4;
AC O938P4;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Pyrogenic exotoxin A (Fragment).
GN Name=speA;
OS Streptococcus equisimilis.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCB1_TaxID=119602;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22508029; PubMed=1620634;
RA Kalia A., Bessen D.E.;
RT "Presence of streptococcal pyrogenic exotoxin A and C genes in human
RT isolates of group G streptococci.";
RL FEMS Microbiol. Lett. 219:291-295(2003).
DR EMBL; AY049745; AAL06068.1; -.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
```



```

DR InterPro: IPR006177; Bcstr1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox_08.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 222;
Best Local Similarity 33.8%; Pred. No. 7,7e-15;
Matches 75; Conservative 41; Mismatches 95; Indels 11; Gaps 7;

QY 4 SEINEKDLRKSELORNAL-SNLROIY--YYNEKAITENKESDDOFLNTLLFKGFTG 60
DB 5 SEVEFPAQDPNPFSQLRRSSLVKNLQNIYFLYEGDPVHENVKSVDDLSHDLIYN--VS 61
QY 61 HPWYNDLVLVDLSKQATNKYKGVLDYGAYYGQC-AGTNPNTACMTGGVTLHDNNRL 119
DB 62 GLNYDLKTELKRNREMSLTFKKNQVDIYGEVEYYHGYLCRNKRRACTIYGVTNHGNNL 121
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKVTYQVELDQARHYLHGKFGLYNSDSFGKY 179
DB 122 ELPKNIILVAVSIDG10-SLSPD-IEFSKGMVTAQELDYKVRKRLTNNQLYTNGP--SKY 177
QY 180 ORGLIVFHSSEGSTVSYDLFDAQGYPTLRLIRYDNKTINS 221
DB 178 ETGYIKFISKDKETFWDFPPEPFQVQKYLMIYKNEITLDS 219

RESULT 85
Q9RSZ4 PRELIMINARY; PRT; 222 AA.
AC Q9RSZ4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Ecotoxin type A (Fragment).
GN Name=spA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_Taxid=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D633;
RX MEDLINE=99137798; PubMed=9952369;
RA Beesen D.E., Izzo M.W., Fiorentino T.R., Caringal R.M.,
RA Hollingshead S.K., Beall B.;
RT "Genetic linkage of ecotoxin alleles and emm gene markers for tissue
RT tropism in group A streptococci.";
RL J. Infect. Dis. 179:627-636 (1999).
DR EMBL; AF029051; AAD21315.1; -.
DR HSSP; P01552; ISEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox_08.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 222
SQ SEQUENCE 222 AA; 25884 MW; 121F8460992818F8 CRC64;

```

```

Query Match 22.4%; Score 277.5; DB 2; Length 222;
Best Local Similarity 33.8%; Pred. No. 7,7e-15;
Matches 75; Conservative 41; Mismatches 95; Indels 11; Gaps 7;

QY 4 SEINEKDLRKSELORNAL-SNLROIY--YYNEKAITENKESDDOFLNTLLFKGFTG 60
DB 5 SEVEFPAQDPNPFSQLRRSSLVKNLQNIYFLYEGDPVHENVKSVDDLSHDLIYN--VS 61
QY 61 HPWYNDLVLVDLSKQATNKYKGVLDYGAYYGQC-AGTNPNTACMTGGVTLHDNNRL 119
DB 62 GLNYDLKTELKRNREMSLTFKKNQVDIYGEVEYYHGYLCRNKRRACTIYGVTNHGNNL 121
QY 120 TEKKVPINLWIDGKQTTVPIDKVTSKKVTYQVELDQARHYLHGKFGLYNSDSFGKY 179
DB 122 ELPKNIILVAVSIDG10-SLSPD-IEFSKGMVTAQELDYKVRKRLTNNQLYTNGP--SKY 177
QY 180 ORGLIVFHSSEGSTVSYDLFDAQGYPTLRLIRYDNKTINS 221
DB 178 ETGYIKFISKDKETFWDFPPEPFQVQKYLMIYKNEITLDS 219

RESULT 86
Q9RSX4 PRELIMINARY; PRT; 234 AA.
AC Q9RSX4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE ENTEROTOXIN=PYROGENIC toxin (Fragment).
OS Staphylococcus.
OC Bacteria; Firmicutes; Bacillales.
OX NCBI_Taxid=1279;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94325995; PubMed=8049778; DOI=10.1006/mpcv.1993.1027;
RA Van den Bussche R.A., Lyon J.D., Bohach G.A.;
RL Mol. Phylogenet. Evol. 2:281-292 (1993).
DR HSSP; P34071; 114X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact1 tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_tox_08.
DR InterPro: IPR006173; Staph_tox_08.
DR Pfam: PF01123; Staph_strep_toxin; 1.
DR Pfam: PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT NON_TER 234
SQ SEQUENCE 234 AA; 27122 MW; D6A7B45FB9810052 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 234;
Best Local Similarity 31.6%; Pred. No. 8,2e-15;
Matches 74; Conservative 49; Mismatches 92; Indels 19; Gaps 9;

QY 11 DLARKSELORNALSNLROIYYNEKAITENK-ESDDOFLNTLLFKGFTGHPWYNDLVL 69
DB 5 DLHKSSEF-TGTVGNMK--LYLDNVYSAIKVSVDFLAHDLIYNSDRLKNYDKVKT 61
QY 70 DLGSKDATNKYKGVLDYGAYYGQC-----AGTNPNTACMTGGVTLHDNNRLTEB 122
DB 62 ELINEDLAKKYKDEVDVGSNYVNCYFSSKONVGKVTGKTCMTGAGITKHGNNHNDG 121
QY 123 --KKVPINLWIDGKQTTVPIDKVTSKKVTYQVELDQARHYLHGKFGLYNSDSFGKY 180
DB 122 NLQNVIVRVY-ENKRTITSE-VQTDKSVTAQELDIKANNFLINKNLTEFNS--SPYE 177
QY 181 RGLIVFHSSEGSTVSYDLFDAQGYPTLRLIRYDNKTINSNLHDLIYLT 232

```

Db 178 TGYIKFIENNFTFWYDMWPAFGDKFDQSKYIMMYNDKNTXDSKSVKIEVHLTT 231

RESULT 87

OS4779 PRELIMINARY; PRT; 236 AA.

ID OS4779; OS4613; OS4736; OS4740; OS4741;

AC OS4779; OS4613; OS4736; OS4740; OS4741; Created

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)

DE Type A exotoxin precursor (Fragment).

GN Name=spea;

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MGAS485; MGAS158; MGAS491; MGAS495; and MGAS624;

RX MEDLINE=92044323; PubMed=1940804;

RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;

RT "Characterization and clonal distribution of four alleles of the speA gene encoding pyrogenic exotoxin A (scarlet fever toxin) in Streptococcus pyogenes.";

RL J. Exp. Med. 174:1271-1274(1991).

DR EMBL; X61569; CAA43767.1; -

DR EMBL; X61568; CAA43766.1; -

DR EMBL; X61570; CAA43768.1; -

DR EMBL; X61571; CAA43769.1; -

DR EMBL; X61572; CAA43770.1; -

DR PIR; A60108; A60108.

DR HSSP; P01552; 1SERB.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bactr_tox.

DR InterPro; IPR006123; Staph/Strep_toxin.

DR InterPro; IPR006126; Staph/Strep_tox.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF01123; Staph_strep_toxin; 1.

DR Pfam; PF02876; Staph_strep_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

KW signal.

FT NON_TER

FT SIGNAL

FT CHAIN

FT NON_TER

SQ SEQUENCE 236 AA; 27468 MW; 29DF2AD575623A84 CRC64;

Query Match 22.4%; Score 277.5; DB 2; Length 236;

Best Local Similarity 33.3%; Pred. No. 8.3e-15;

Matches 77; Conservative 44; Mismatches 91; Indels 19; Gaps 10;

Db 4 SEINEKDLRKKSSELRNAL-SNLKQIYY-YNEKAIT-ENKESDQPLENTLLFKGFPTG 60

Db 17 SOEVAQODPPPSQHRSSLVKLNQNIYFLYEGDPVTHENVKSVQQLSHDLIV---VS 73

Qy 61 HPWYNDLVLDGSKATNKYKGVLDYGAIVGYQC-AGTTPNKTAQMGVGTLLHDNR 119

Db 74 GPNYDKLTTELKNGEMATLFDKKNIDIVGEVYHLCYLCENAERSACIYGVGTNHEGNHL 133

Qy 120 TEEKVPINLWIDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKGLVNSDSFGSKV 179

Db 134 EIPKTIIVKVSIDGQ-SLSFD-IETNKMTVAQELDYKRYKLYLDNKQLYNGP--SKY 189

Qy 180 QRGILVFHSSSEGSTVSYDLFD---AQGOYPTLLRIYRDNKTINSENLHI 226

Db 190 ETGYIKFIIPKNKESFWFDFPPEPFTQSKY---LMITYDNMTLDSNNSQI 236

RESULT 88

Q9R931

ID Q9R931 PRELIMINARY; PRT; 222 AA.

AC Q9R931;

DT 01-MAY-2000 (TREMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBLrel. 13, last sequence update)

DT 01-OCT-2003 (TREMBLrel. 25, last annotation update)

DE Exotoxin A (Fragment).

GN Name=spea;

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

OX NCBI_TaxID=1314;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=D709;

RX MEDLINE=99137798; PubMed=9952369;

RA Bessen D.E., Izso M.W., Fiorentino T.R., Carling R.M., Hollingshead S.K., Beall B.;

RT "Genetic linkage of exotoxin alleles and emm gene markers for tissue tropism in group A streptococci.";

RL J. Infect. Dis. 179:627-636 (1999).

DR EMBL; AF055698; AAD11624.1; -

DR PIR; A60108; A60108.

DR HSSP; P01552; 1SERB.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0009405; P:pathogenesis; IEA.

DR InterPro; IPR008992; Bact_endotox.

DR InterPro; IPR006177; Bactr_tox.

DR InterPro; IPR006123; Staph/Strep_toxin.

DR InterPro; IPR006126; Staph/Strep_tox.

DR InterPro; IPR006173; Staph_tox_OB.

DR Pfam; PF01123; Staph_strep_toxin; 1.

DR Pfam; PF02876; Staph_strep_toxin; 1.

DR PRINTS; PR00279; BACTRLTOXIN.

DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.

DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.

FT NON_TER

FT NON_TER

SQ SEQUENCE 222 AA; 25759 MW; 48BB7ADDCD91FBA3 CRC64;

Query Match 22.3%; Score 276.5; DB 2; Length 222;

Best Local Similarity 34.1%; Pred. No. 9.3e-15;

Matches 77; Conservative 43; Mismatches 87; Indels 19; Gaps 10;

Db 4 SEINEKDLRKKSSELRNAL-SNLKQIYY-YNEKAIT-ENKESDQPLENTLLFKGFPTG 60

Db 5 SOEVAQODPPPSQHRSSLVKLNQNIYFLYEGDPVTHENVKSVQQLSHDLIV---VS 61

Qy 61 HPWYNDLVLDGSKATNKYKGVLDYGAIVGYQC-AGTTPNKTAQMGVGTLLHDNR 119

Db 62 GPNYDKLTTELKNGEMATLFDKKNIDIVGEVYHLCYLCENAERSACIYGVGTNHEGNHL 121

Qy 120 TEEKVPINLWIDGQTTVPIDKVTSKKEVTVOELDQARHYLHGKGLVNSDSFGSKV 179

Db 122 EIPKTIIVKVSIDGQ-SLSFD-IETNKMTVAQELDYKRYKLYLDNKQLYNGP--SKY 177

Qy 180 QRGILVFHSSSEGSTVSYDLFD---AQGOYPTLLRIYRDNKTINS 221

Db 178 ETGYIKFIIPKNKESFWFDFPPEPFTQSKY---LMITYDNMTLDS 219

RESULT 89

OS7453

ID OS7453 PRELIMINARY; PRT; 236 AA.

AC OS7453;

DT 01-NOV-1996 (TREMBLrel. 01, Created)

DT 01-NOV-1996 (TREMBLrel. 01, last sequence update)

DT 05-JUL-2004 (TREMBLrel. 27, last annotation update)

DE Type A exotoxin precursor (Fragment).

GN Name=spea;

OS Streptococcus pyogenes.

OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

OC Streptococcus.

```

OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS156, MGAS250, MGAS256, MGAS285, MGAS480, MGAS492, and
RC MGAS496;
RX MEDLINE=92044323; PubMed=1940804;
RA Nelson K., Schlievert P.M., Seldner R.K., Musser J.M.;
RT "Characterization and clonal distribution of four alleles of the speA
RT gene encoding pyrogenic exotoxin A (scarlet fever toxin) in
RT Streptococcus pyogenes.";
RL J. Exp. Med. 174:1271-1274(1991).
DR EMBL; X61562; CAA43760.1; -
DR EMBL; X61561; CAA43759.1; -
DR EMBL; X61563; CAA43761.1; -
DR EMBL; X61564; CAA43762.1; -
DR EMBL; X61565; CAA43763.1; -
DR EMBL; X61566; CAA43764.1; -
DR EMBL; X61567; CAA43765.1; -
DR PIR; A60108; A60108.
DR HSSP; P01552; 1SEB.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
KW Signal
FT NON_TER
FT SIGNAL
FT CHAIN
FT NON_TER
SQ SEQUENCE 236 AA; 27484 MW; 2E7F41AAC853600 CRC64;

Query Match 22.0%; Score 272.5; DB 2; Length 236;
Best Local Similarity 33.3%; Pred. No. 2.1e-14;
Matches 77; Conservative 43; Mismatches 92; Indels 19; Gaps 10;

QY 4 SEIRNKDLRKSELOQNAL-SNLROIYY-YNEKAIT-ENKESDDOFLNTLLFKGFFTG 60
DB 17 SQEVFAQODPDPQLHSSSLVKNLQNYFLYEGDPVTHENVKSYDQLSHDLIYN--VS 73
QY 61 HPWYNDLVDLGSKDATNKYKGGKVDLYGAYGYQC-AGGTPNKTAQMGYVTLHDNNRL 119
DB 74 GPVYDLKTKLKNQEMATLFDKNVDIYSEYHLCYLCENABRSACIYGGVTNHEGNHL 133
QY 120 TEEKVQPINIMIDGKQTTVPIDKYKTSKKEVTVQELDQARHYLHGKFGLYNSDSFGGKV 179
DB 134 EIRPKTIYVVKISIGIQ-SLSFPD-IETKKQVTAQELDYKRAKYLTDKQKQLYTNGP--SKY 189
QY 180 QRLGIYHSESGSTVSVDLFD---AGQVPTLIRYRNKNTINSENLHI 226
DB 190 ETGYIKFIPKNKESFWDFPPEFTQSKY---LMIYKQNETLDSNTSQI 236

RESULT 90
ID Q06534 PRELIMINARY; PRT; 239 AA.
AC Q06534;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TEMBLrel. 25, Last annotation update)
DE Enterotoxin (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RX MEDLINE=94011313; PubMed=8406814;
RA Marx J.C., Lyon J.D., Roberson J.R., Lupter M., Bohach G.A.;
RT "Characterization of novel type C staphylococcal enterotoxins:
RT biological and evolutionary implications.";
RL Infect. Immun. 61:4254-4262(1993).
DR EMBL; U13379; AAA26623.1; -
DR HSSP; P34071; 114X.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactr_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_strep_toxin; 1.
DR Pfam; PF02876; Staph_strep_tox_C; 1.
DR PRINTS; PR00279; BACTRTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER
SQ SEQUENCE 239 AA; 27517 MW; F354742619C8D196 CRC64;

Query Match 22.0%; Score 272.5; DB 2; Length 239;
Best Local Similarity 30.5%; Pred. No. 2.2e-14;
Matches 74; Conservative 52; Mismatches 98; Indels 19; Gaps 9;

QY 2 EKESEINERDLRKSELOQNALSNLROIYYNEKAITENK-ESDDOFLNTLLFKGFFTG 60
DB 1 ESQPDPTPELHKASGF-TGLMENNMYL--YDRIYSAIKVYSVDFLHDLIYISDKK 57
QY 61 HPWYNDLVDLGSKDATNKYKGGKVDLYGAYGYQC-----AGGTPNKTAQMGYVTL 113
DB 58 LKNYDKYKTEILNEDIAKKYKDEVVDVGSNNYVNCFFSSKDNVGVGTGKTCMYGKITK 117
QY 114 HDNNRLTEE-KKVPINIMIDGKQTTVPIDKYKTSKKEVTVQELDQARHYLHGKFGLYN 171
DB 118 HEGNHDFDNGNLQVNLRLRYV-ENKRNITSE-VQTDKSVTAQELDKAASFLLNKNKLYE 175
QY 172 SDSFGKVQVQGLVHFSSSEGSTVSVDLPDAQGYPD--TLIRYRNKNTINSENLHI 229
DB 176 FNS-SPEYTGTYKFIENNNGNTYWMMPAGBDFQSKYLMYNNKNTYDSVSLIEVH 233
QY 230 LYT 232
DB 234 LTT 236

RESULT 91
ID Q54971 PRELIMINARY; PRT; 260 AA.
AC Q54971;
DT 01-NOV-1996 (TEMBLrel. 01, Created)
DT 01-NOV-1996 (TEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
DE Superantigen.
GN Name=SSA;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
AC MEDLINE=94222556; PubMed=8168951;
RX Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal superantigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
DR EMBL; U29565; AAA65928.1; -
DR PDB; 1BXT; X-ray; A/B=27-260.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.

```

DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006173; Bactrl_tox.
DR InterPro; IPR006126; Staph/Strep_toxin.
DR InterPro; IPR006173; Staph/Strep_tox.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29757 MW; 2DD96017DE9DAF49 CRC64;

Query Match 21.8%; Score 269.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 4.3e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELRNALSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
DB 35 EQLN-----KSSQFTGVGNLRCL-YDNHFEVETNVASTQQLQHDLIFFPKDKLKNY 87
QY 65 NDILVDLGSKDATNKKKQKVDLYGAYYGOCAGTPTN-----KTACWYGVTLLHDNRRL 119
DB 88 DSVKTEFNSKDLATKTKKQKVDIFGSNYYNYCYSEGSCKNAKTKCMYGVTTEHHRQI 147
QY 120 TEEKKVPINLWI---DGKQTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
DB 148 --EGKFP-NITVKKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKULVEFFN-- 201

QY 177 GKVRGLVPHSSSESTVSYDLFDAGQGYPD--TLRLRYDNKKTINSENLHIDLTL 230
DB 202 SPYETGYIKFTLESSGDSFWMMPAPGALFDQSKYLMYLNDRKTVSSSAIAIEVHL 257

RESULT 92

ID 054738 PRELIMINARY; PRT; 260 AA.

AC 054738;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Superantigen SSA.
GN Name=ssa;
GN Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RT "Molecular characterization and phylogenetic distribution of the
streptococcal superantigen gene (ssa) from Streptococcus pyogenes.",
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 1842;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.,
RT "Phylogenetic distribution of streptococcal superantigen SSA allelic
variants provides evidence for horizontal transfer of ssa within
Streptococcus pyogenes.",
RL Infect. Immun. 64:1161-1165(1996).
DR EMBL; U48793; AA802149.1; -.
DR HSSP; O54871; IBXT.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_Strep_tox_C; 1.

DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29836 MW; C122151633B42AD6 CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELRNALSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
DB 35 EQLN-----KSSQFTGVGNLRCL-YDNHFEVETNVASTQQLQHDLIFFPKDKLKNY 87
QY 65 NDILVDLGSKDATNKKKQKVDLYGAYYGOCAGTPTN-----KTACWYGVTLLHDNRRL 119
DB 88 DSVKTEFNSKDLATKTKKQKVDIFGSNYYNYCYSEGSCKNAKTKCMYGVTTEHHRQI 147
QY 120 TEEKKVPINLWI---DGKQTVPIDKVTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
DB 148 --EGKFP-NITVKKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKULVEFFN-- 201

QY 177 GKVRGLVPHSSSESTVSYDLFDAGQGYPD--TLRLRYDNKKTINSENLHIDLTL 230
DB 202 SPYETGYIKFTLESSGDSFWMMPAPGALFDQSKYLMYLNDRKTVSSSAIAIEVHL 257

RESULT 93

ID 079X14 PRELIMINARY; PRT; 260 AA.

AC 079X14;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE SSA.
GN OrderedLocusNames=SPB1119;
OS Streptococcus pyogenes (serotype M3).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=198466;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SSI-1;
RX MEDLINE=22683278; PubMed=12799345; DOI=10.1101/gr.1096703;
RA Nakagawa I., Kurokawa K., Yamashita A., Nakata M., Tomiyasu Y.,
RA Okahashi N., Kawabata S., Yamazaki K., Shida T., Yasunaga T.,
RA Hayashi H., Hattori M., Hamada S.;
RT "Genome sequence of an M3 strain of Streptococcus pyogenes reveals a
large-scale genomic rearrangement in invasive strains and new insights
into phage evolution.",
RL Genome Res. 13:1042-1055 (2003).
DR EMBL; AP005144; BAC64214.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactrl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_Strep_tox_C; 1.
DR Pfam; PF01123; Staph_Strep_toxin; 1.
DR Pfam; PF02876; Staph_Strep_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29767 MW; EALFBYCAE80P998 CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best Local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservative 37; Mismatches 98; Indels 23; Gaps 9;

QY 5 EINEKDLRKSELRNALSLRQIYYNEKAITENKESDDQFLNTLTLFKGFTGHWPY 64
DB 35 EQLN-----KSSQFTGVGNLRCL-YDNHFEVETNVASTQQLQHDLIFFPKDKLKNY 87

```
Db      35 EOLN-----KSSQFTGWGNLRCL-YDNHFVEGTVNRSTGQLDQHDLPFIKDLKKNY 87
Qy      65 NDLDVLDGSKDATNKKYKGVLDYGAAYGYQACGTPN-----KTACMGVGTLLDNNRL 119
Db      88 DSVKTEFNSKDLAAKYKNKDVIDFGSNYYNYCYSEGNSCNNAKTCMVGTEHHRNDI 147
Qy      120 TEKKVPINLWI---DGKQTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
Db      148 --EGKFP-NITVKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKNLYERN-- 201
Qy      177 GKVQGLIVFHSSEGSTVSYDLFDAGQGYPD--TLRIYRDNKNTINSNLHIDLVL 230
Db      202 SPYENGVIKFISSGDSFWYDMMAPGALFDQSKYLMYNDKVTSSSAIAIEVHL 257

RESULT 94
054739 PRELIMINARY; PRT; 260 AA.
ID 054739; 054737;
AC 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
DE Supranatigen SSA.
GN Name=ssa;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxId=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 58;
RX MEDLINE=94222556; PubMed=8168951;
RA Reda K.B., Kapur V., Molllick J.A., Lamphear J.G., Musser J.M.,
RA Rich R.R.;
RT "Molecular characterization and phylogenetic distribution of the
RT streptococcal supranatigen gene (ssa) from Streptococcus pyogenes.";
RL Infect. Immun. 62:1867-1874(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=MGAS 58;
RX MEDLINE=96178602; PubMed=8606073;
RA Reda K.B., Kapur V., Goela D., Lamphear J.G., Musser J.M., Rich R.R.;
RT "Phylogenetic distribution of streptococcal supranatigen SSA allelic
RT variants provides evidence for horizontal transfer of ssa within
RT Streptococcus pyogenes.";
RL Infect. Immun. 64:1161-1165(1996).
DR EMBL: U48794; AAB02150.1; -
DR EMBL: U48793; AAB02148.1; -
DR HSSP: Q54971; IBXT.
DR GO: 0005576; C:extracellular; IEA.
DR GO: 0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_toxin_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 260 AA; 29767 MW; EAIFB7CCAB80F99B CRC64;

Query Match 21.6%; Score 267.5; DB 2; Length 260;
Best local Similarity 33.1%; Pred. No. 6.2e-14;
Matches 78; Conservativity 37; Mismatches 96; Indels 23; Gaps 9;

Qy      5 EINEKDLRKKSLEIQRNALSNLRQIYYNEKATENKESDDQFLNLTLEKFGFTGHPWY 64
Db      35 EOLN-----KSSQFTGWGNLRCL-YDNHFVEGTVNRSTGQLDQHDLPFIKDLKKNY 87
Qy      65 NDLDVLDGSKDATNKKYKGVLDYGAAYGYQACGTPN-----KTACMGVGTLLDNNRL 119
```

```
Db      88 DSVKTEFNSKDLAAKYKNKDVIDFGSNYYNYCYSEGNSCNNAKTCMVGTEHHRNDI 147
Qy      120 TEKKVPINLWI---DGKQTVPIDKVKTSKKEVTVOELDQARHYLHGKFGLYNSDSFG 176
Db      148 --EGKFP-NITVKYEDNENILSPD-ITTNKKQVTVQELDCKTRKILVSRKNLYERN-- 201
Qy      177 GKVQGLIVFHSSEGSTVSYDLFDAGQGYPD--TLRIYRDNKNTINSNLHIDLVL 230
Db      202 SPYENGVIKFISSGDSFWYDMMAPGALFDQSKYLMYNDKVTSSSAIAIEVHL 257

RESULT 95
ETCL STAAU STANDARD; PRT; 266 AA.
ID ETCL STAAU
AC P01553;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Enterotoxin type C-1 precursor (SEC1).
GN Name=etC1;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxId=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88038352; PubMed=2823067;
RA Bohach G.A., Schlievert P.M.;
RT "Nucleotide sequence of the staphylococcal enterotoxin C1 gene and
RT relatedness to other pyrogenic toxins.";
RL Mol. Gen. Genet. 209:15-20(1987).
RN [2]
RP SEQUENCE OF 28-266.
RX MEDLINE=83213327; PubMed=6189824;
RA Schmidt J.U., Spero L.;
RT "The complete amino acid sequence of staphylococcal enterotoxin C1.";
RL J. Biol. Chem. 258:6300-6306(1983).
CC -1- FUNCTION: Staphylococcal enterotoxins cause the intoxication
CC staphylococcal food poisoning syndrome. The illness characterized
CC by high fever, hypotension, diarrhea, shock, and in some cases
CC death.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the staphylococcal/streptococcal toxin
CC family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X05815; CAA29260.1; -
DR S06356; ENSACI.
DR HSSP: P34071; 114X.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bactl_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006126; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF02876; Staph_Strep_toxin_C_1.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Direct protein sequencing; Enterotoxin; Signal; Supranatigen; Toxin.
FT CHAIN 1 27 Enterotoxin type C-1.
FT DISULFID 120 137
FT CONFLICT 177 177 D -> N (in Ref. 2).
SQ SEQUENCE 266 AA; 30546 MW; 3A7AB59A896853B CRC64;

Query Match 21.5%; Score 266.5; DB 1; Length 266;
```

Best Local Similarity 30.5%; Pred. No. 7.7e-14;
Matches 74; Conservative 51; Mismatches 101; Indels 17; Gaps 8;

QY 1 SEKSEINEKDLRKSELOARN--ALSNIHQIYY--YNEKAITENKESDDOFLENTLLFKGFTG 60
DB 27 AESQDPPFPELHAKSKF--TGLMNMKVLVDHYSAIKYK--SVKFLAHLDIYISDK 84
QY 61 HPWYNDLLVDLSKDATNKYKGVLDYGAAYGYOC-----AGTPNKACMYGVTL 113
DB 85 LKNVDKVTLELNEGAKKYKDEVVDYGSNYVNCYFSSKDNVGMKVTGKTCMYGGITK 144
QY 114 HDNRRLTEE--KKVYINMIDGKQTTVPIDKTKSKETVQELDQARHYLHGKFGLYN 171
DB 145 HEGNHFNDGNLQNVILIRY--ENKRTISFE--VQTKKSVTAQELDIKANFLINKNLYE 202
QY 172 SDSFGKVGRLIVFHSSEGSTVSYDLFDAQGYPDT--TLRIYRDNKTTINSENLHIDY 229
DB 203 FNS--SPETGYIKTEINNGNTFWIDMMPAPGDKPDQSKYLMYDNKTVDSKSYKIEVH 260
QY 230 LYT 232
DB 261 LTT 263

RESULT 96
Q6GFN2 PRELIMINARY; PRT; 258 AA.
AC Q6GFN2;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin.
GN OrderedLocustNames=SA1916;
OS Staphylococcus aureus (strain MRSA252).
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=282458;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=15213324; DOI=10.1073/pnas.0402521101;
RA Holden M.T.G., Fell E.J., Lindsey J.A., Peacock S.J., Day N.P.J.,
RA Enright M.C., Foster T.J., Moore C.E., Hurst L., Aklin R., Barron A.,
RA Baon N., Bentley S.D., Chillingworth C., Chillingworth T.,
RA Churcher C., Clark L., Cotton C., Cronin A., Doggett J., Dowd L.,
RA Fellwell T., Hance Z., Harris B., Hauser H., Holtroyd S., Jagsels K.,
RA James K.D., Lennard M., Line A., Mayes R., Mowle S., Mungall K.,
RA Omond D., Quail M.A., Rabinowitch E., Rutherford K.M., Sanders M.,
RA Sharp S., Simmonds M., Stevens K., Whitehead S., Whitehead B.G.,
RA Spratt B.G., Parkhill J.;
RT "Complete genomes of two clinical Staphylococcus aureus strains:
RT evidence for the rapid evolution of virulence and drug resistance.";
RL Proc. Natl. Acad. Sci. U.S.A. 101:9786-9791(2004).
DR EMBL: BX571856; CAG40902.1; -
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_toxin_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
KW Complete proteome.
SQ SEQUENCE 258 AA; 29855 MW; 722C8517945DDFES CRC64;

Query Match 21.4%; Score 264.5; DB 2; Length 258;
Best Local Similarity 29.5%; Pred. No. 1.1e-13;
Matches 75; Conservative 51; Mismatches 85; Indels 43; Gaps 12;

QY 1 SEKSEINEKDLRKSELOARN--ALSNIHQIYY--YNEKAITENKESDDOFLENTLLFK 55
DB 25 SQDPKIDE--LNKSDYKSNKGTGNWNLVMSPPVSGRGVINSR----QFLSHDLIFP 78

QY 56 GFTGHPYNDLLVDLSKDATNKYKGVLDYGAAYGYOC-----GTPNK 103
DB 79 ---IEYKSEINEKDLRKSELOARN--ALSNIHQIYY--YNEKAITENKESDDOFLENTLLFK 131
QY 104 TACWYGVTLH--DNRRLTEERKVPINLMIDGKQTTVPIDKTKSKETVQELDQARHYLHGKFG 161
DB 132 -CMYGGIYFNSSENER--DKLIVQVTLIDNRQSLG--FITTKKNNVTLQELDYKARH 185
QY 162 YLHGKFGLYNSDSFGKVGRLIVFHSSEGSTVSYDLFDAQGYPDT--TLRIYRDNK 218
DB 166 WLTEKKLYEPD--GSAPESGYIKTEKNTSFWFDLPKKELVFPVYKFLNIYGDNKV 243
QY 219 INSENLHIDLYT 232
DB 244 VDSKIKMEVPLNT 257

RESULT 97
Q9ZNF2 PRELIMINARY; PRT; 258 AA.
AC Q9ZNF2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Enterotoxin type Gv.
GN Name=seg2;
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
CX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20260630; PubMed=10803494;
RA Abe J., Ito Y., Onimaru M., Kohsaka T., Takeda T.;
RT "Characterization and distribution of a new enterotoxin-related
RT superantigen produced by Staphylococcus aureus.";
RL Microbiol. Immunol. 44:79-88(2000).
DR EMBL: AB016487; BA36693.1; -
DR HSP; P01552; ISEB.
DR GO: GO:0005576; C:extracellular; IEA.
DR GO: GO:0009405; P:pathogenesis; IEA.
DR InterPro: IPR008992; Bact_endotox.
DR InterPro: IPR006177; Bact_tox.
DR InterPro: IPR006123; Staph/Strep_toxin.
DR InterPro: IPR006173; Staph/Strep_toxin.
DR Pfam: PF01123; Staph_Strep_toxin_1.
DR Pfam: PF02876; Staph_Strep_toxin_C_1.
DR PRINTS: PR00279; BACTRLTOXIN.
DR PROSITE: PS00278; STAPH_STREP_TOXIN_2; 1.
SQ SEQUENCE 258 AA; 29839 MW; 1229246D83F4FB77 CRC64;

Query Match 21.2%; Score 262.5; DB 2; Length 258;
Best Local Similarity 29.5%; Pred. No. 1.6e-13;
Matches 72; Conservative 49; Mismatches 82; Indels 41; Gaps 11;

QY 11 DIRKSELOARN--ALSNIHQIYY--YNEKAITENKESDDOFLENTLLFKGFTGHPYN 65
DB 33 ELNKVSDYKSNKGTGNWNLVMSPPVSGRGVINSR----QFLSHDLIFP--IEYKSN 85
QY 66 DLYVDLSKDATNKYKGVLDYGAAYGYOC-----GTPNKACMYGVTL 113
DB 86 EYKTELENTLANNYKGVLDYGAAYGYOC-----GTPNKACMYGVTL 140
QY 114 H--DNRRLTEERKVPINLMIDGKQTTVPIDKTKSKETVQELDQARHYLHGKFGLYN 171
DB 141 NSSENER--DKLIVQVTLIDNRQSLG--FITTKKNNVTLQELDYKARHWTKEKKLYE 195
QY 172 SDSFGKVGRLIVFHSSEGSTVSYDLFDAQGYPDT--TLRIYRDNKTTINSENLHIDY 228
DB 196 FD--GSAPESGYIKTEKNTSFWFDLPKKELVFPVYKFLNIYGDNKVYDSKIKMEV 253
QY 229 YLYT 232
DB 254 FLNT 257

```

RESULT 98
Q6XZET7 PRELIMINARY; PRT; 222 AA.
AC Q6XZET7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin sec variant (Fragment).
OS Staphylococcus aureus.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1280;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3528;
RX MEDLINE=22943091; PubMed=14580397; DOI=10.1016/S0890-8508(03)00058-6;
RA Letertre C., Perelle S., Dillasser F., Fach P.;
RT "A strategy based on 5' nuclease multiplex PCR to detect enterotoxin
genes sea to sea of Staphylococcus aureus.";
RL Mol. Cell. Probes 17:227-235(2003).
DR EMBL; AY196688; AAP37185.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; 1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1.
FT NON_TER 1
FT TER 222
SQ SEQUENCE 222 AA; 25784 MW; 67A0546FF3CD73B1 CRC64;

Query Match 21.0%; Score 259.5; DB 2; Length 222;
Best Local Similarity 31.0%; Pred. No. 2,3e-13;
Matches 70; Conservative 48; Mismatches 89; Indels 19; Gaps 9;

QY 11 DLKKELEQNALSNLRQIYYNEKAITENK-ESDDQPLENTLLFKGFTGHPMYNDLIV 69
DB 3 ELHKASKF-TGLMNMKVLT--YDRYVSATKVSVDLFHLADLIYINSDKKLKNYDKVKT 59
QY 70 DLGSKDATNKKYKGGKVDLYGAYGYOC-----AGTTPNKTAQMYGGVTLHDNNRLTEE 122
DB 60 ELLNEELAKKYKQEVVDVGSNYVANCYFSKDNVGVKVTGKTCMVGITKHSGNHPDNG 119
QY 123 K-KVPINLMIDKQTTVPIDKYTKSKVEYTVQELDQARHYLHGKFGLYNSDSFGGKVKQ 180
DB 120 KLONVILRVY-ENKRNLTISPE-VQTDKSVTAQELDIKANKLFLINKKLTLEFNS--SPYE 175
QY 181 KGLIVHSSGSGTVSYDLFDAGOC--YPTLLRIYRNKNTINSENL 224
DB 176 TGXIKFIENNGNTFWYDMPAPDQKREQSKYLLMYNNDKNTVDSKSV 221

RESULT 99
Q764P6 PRELIMINARY; PRT; 264 AA.
AC Q764P6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Enterotoxin precursor.
OS Name=se-int;
OS Staphylococcus intermedius.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1285;
RN [1]
RP SEQUENCE FROM N.A.

```

```

RC STRAIN=AV8004;
RA Futagawa-Saito K., Suzuki M., Ohsawa M., Ohshima S., Sakurai N.,
RA Ba-Thein W., Fukuyasu T.;
RT "Identification and prevalence of an enterotoxin-related gene, se-int,
RT in Staphylococcus intermedius isolates from dogs and pigeons.";
RL J. Appl. Microbiol. 96:1361-1366(2004).
DR EMBL; AB116378; BAD13763.1; -.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.
DR InterPro; IPR006123; Staph/Strep_toxin.
DR InterPro; IPR006126; Staph/Strep_tox.
DR InterPro; IPR006173; Staph_tox_OB.
DR Pfam; PF01123; Staph_stp_toxin; 1.
DR Pfam; PF02876; Staph_stp_tox_C; 1.
DR PRINTS; PR00279; BACTRLTOXIN.
DR PROSITE; PS00277; STAPH_STREP_TOXIN_1; UNKNOWN_1.
DR PROSITE; PS00278; STAPH_STREP_TOXIN_2; 1..
KM Signal.
FT SIGNAL 1
FT CHAIN 28 27 Potential.
FT SEQUENCE 264 AA; 30532 MW; 52330A55B4CE0E2F CRC64;

Query Match 20.7%; Score 256.5; DB 2; Length 264;
Best Local Similarity 31.0%; Pred. No. 5,1e-13;
Matches 71; Conservative 39; Mismatches 104; Indels 15; Gaps 6;

QY 12 LKKELEQNALSNLRQIYYNEKAITENK-ESDDQPLENTLLFKGFTGHPMYNDLIV 70
DB 38 LHKSEF-KGLMGNVY--LYDRNPFISESNVSTIDSLADLIIFCIRESSEIKYGLVKT 94
QY 71 LGSKDATNKKYKGGKVDLYGAYGYOC-----AGTTPNKTAQMYGGVTLHDNNRLTEE 123
DB 95 FASKELAQKTRNKQVDIFGANYVANCYFSGKGEKNEEDGKTCMVGATVYBGNHLDNHK 154
QY 124 KVPINLMIDKQTTVPIDKYTKSKVEYTVQELDQARHYLHGKFGLYNSDSFGGKVKQ 183
DB 155 SQTIYKVFENSCHITTFELQDKLVTAQELDQARKKFLIDKLNLY--EFKSPYETGY 212
QY 184 IYHSSGSGTVSYDLFDAGOC--YPTLLRIYRNKNTINSENLHLYL 230
DB 213 IKFENDDKSFYDLMPPGNNFNQSKYLLTMYSDNKTVESEDIKIVHL 261

RESULT 100
Q9ROO5 PRELIMINARY; PRT; 209 AA.
AC Q9ROO5;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Mucogenic exotoxin Z 2 (Fragment).
GN Name=semeZ-2;
OS Streptococcus pyogenes.
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus.
OX NCBI_TaxID=1314;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2035;
RX MEDLINE=99093428; PubMed=9874566;
RA Proft T., Mofatt S.L., Berkahn C.J., Fraser J.D.;
RT "Identification and characterization of novel superantigens from
RT Streptococcus pyogenes.";
RL J. Exp. Med. 189:89-102(1999).
DR EMBL; AF086626; AAD52087.1; -.
DR PDB; 1ET6; X-ray; A/B=1-209.
DR PDB; 1EJ3; X-ray; A/B=1-209.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0009405; P:pathogenesis; IEA.
DR InterPro; IPR008992; Bact_endotox.
DR InterPro; IPR006177; Bactl_tox.

```

